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OM protein - protein search, using sw model

Run on: July 17, 2003, 19:44:46 ; Search time 20 Seconds  
(without alignments)  
53.442 Million cell updates/sec

Title: US-09-980-177a-12  
Perfect score: 55  
Sequence: 1 ICWGNQLFV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues  
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	505	11	US-09-162-904A-3
2	55	100.0	505	11	US-09-162-904A-4
3	55	100.0	505	11	US-09-824-017-2
4	55	100.0	505	12	US-09-986-118A-2
5	55	100.0	531	12	US-09-991-053-1
6	55	100.0	531	15	US-10-301-260A-1
7	46	83.6	568	12	US-09-991-053-3
8	46	83.6	568	15	US-10-301-260A-3
9	43	78.2	503	11	US-09-822-662-2
10	43	78.2	503	11	US-09-822-662-2
11	40	72.7	794	15	US-10-149-846-2
12	38	69.1	147	12	US-09-764-891-4533
13	38	69.1	1907	11	US-09-832-292-39
14	37	67.3	416	15	US-10-101-464A-937
15	37	67.3	459	15	US-10-156-761-10059
16	35	63.6	29	10	US-09-864-761-40403

17	35	63.6	305	11	US-09-925-300-1194	Sequence 1194, Ap
18	35	63.6	439	15	US-10-176-847-18	Sequence 18, Appl
19	35	63.6	439	15	US-10-177-293-356	Sequence 356, Appl
20	34	61.8	50	10	US-09-864-761-43404	Sequence 43404, A
21	34	61.8	227	15	US-10-264-104-5	Sequence 5, Appl1
22	34	61.8	508	10	US-09-134-377-1	Sequence 1, Appl1
23	34	61.8	508	11	US-09-822-662-1	Sequence 12925, A
24	34	61.8	740	15	US-10-156-761-12925	Sequence 954, Appl
25	34	61.8	1021	15	US-10-101-464A-954	Sequence 68, Appl
26	33	60.0	40	10	US-09-917-340-68	Sequence 6344, Ap
27	33	60.0	76	15	US-10-106-698-6344	Sequence 10607, A
28	33	60.0	122	15	US-10-156-761-10607	Sequence 6229, Ap
29	33	60.0	130	15	US-10-106-698-6229	Sequence 200, Appl
30	33	60.0	186	15	US-10-097-065-341	Sequence 23, Appl
31	33	60.0	330	15	US-10-146-772-200	Sequence 6506, Ap
32	33	60.0	332	12	US-09-557-796-23	Sequence 14394, A
33	33	60.0	376	11	US-09-738-626-6506	Sequence 7, Appl1
34	33	60.0	380	15	US-10-156-761-14394	Sequence 6, Appl1
35	33	60.0	393	10	US-09-836-470B-2	Sequence 7, Appl1
36	33	60.0	393	11	US-09-738-626-5280	Sequence 156, Appl
37	33	60.0	393	12	US-09-494-359-2	
38	33	60.0	393	15	US-10-284-138-2	
39	33	60.0	393	15	US-10-284-334-2	
40	33	60.0	518	12	US-09-881-578-4	
41	33	60.0	548	10	US-09-765-344-6	
42	33	60.0	548	10	US-09-765-344-7	
43	33	60.0	548	15	US-10-288-478-6	
44	33	60.0	548	15	US-10-288-478-7	
45	32	58.2	20	10	US-09-841-133-156	

#### ALIGNMENTS

RESULT 1  
US-09-162-904A-3 ; Sequence 3, Application US/09162904A  
; Patent No. US20020168372A1  
; GENERAL INFORMATION:  
; APPLICANT: Durec, Matthias  
; APPLICANT: Giesmann, Lutz  
; TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE  
; FILE REFERENCE: 8484-068-999  
; CURRENT APPLICATION NUMBER: US/09/162,904A  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/884,168  
; PRIOR FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 08/641,570  
; PRIOR FILING DATE: 1996-05-01  
; PRIOR APPLICATION NUMBER: 08/902,528  
; PRIOR FILING DATE: 1993-07-16  
; SOFTWARE: PatentIn version 3.1  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 3  
; LENGTH: 505  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of L1 ge  
; OTHER INFORMATION: HPV16 Clone  
US-09-162-904A-3

Query Match 100.0%; Score 55; DB 11; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 323 ICWGNQLFV 331

RESULT 2

Mon Jul 21 18:20:13 2003

us-09-980-177a-12.rapb

Page 2

US-09-162-904A-4  
; Sequence 4, Application US/09162904A  
; Patent No. US20020168372A1  
; GENERAL INFORMATION:  
; APPLICANT: Durest, Matthias  
; APPLICANT: Giesmann, Inez  
; TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE  
; OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES  
; FILE REFERENCE: 8864-068-999  
; CURRENT APPLICATION NUMBER: US/09/162,904A  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/884,168  
; PRIOR FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 08/641,570  
; PRIOR FILING DATE: 1996-05-01  
; PRIOR APPLICATION NUMBER: 08/902,528  
; PRIOR FILING DATE: 1993-07-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 4  
; LENGTH: 505  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of L1 get  
US-09-162-904A-4

Query Match 100.0%; Score 55; DB 11; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 ICWGNOLPV 9  
DB 323 ICWGNOLPV 331

RESULT 3  
US-09-824-017-2  
; Sequence 2, Application US/09824017  
; Publication No. US20020197668A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGER, Alexander  
; APPLICANT: HALLEK, Michael  
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
; FORMULATIONS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/824,017  
; FILING DATE: 03-Apr-2001  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/026,896  
; FILING DATE: 1998-02-20  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sandercock, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37067/102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 505 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-824-017-2

Query Match 100.0%; Score 55; DB 11; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 ICWGNOLPV 9  
DB 323 ICWGNOLPV 331

RESULT 4  
US-09-986-118A-2  
; Sequence 2, Application US/09986118A  
; Publication No. US20030021806A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGER, Alexander  
; APPLICANT: HALLEK, Michael  
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
; FORMULATIONS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/986,118A  
; FILING DATE: 07-No. US20030021806A1-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/026,896  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sandercock, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37067/102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 505 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-986-118A-2

Query Match 100.0%; Score 55; DB 12; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 ICWGNOLPV 9  
DB 323 ICWGNOLPV 331

RESULT 5

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US-09-991-053-1
; Sequence 1, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-991-053-1

Query Match          100.0%; Score 55; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9
DB 349 ICWGNOLFFV 357

RESULT 6
US-10-301-260A-1
; Sequence 1, Application US/10301260A
; Publication No. US20030118609A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1123
; CURRENT APPLICATION NUMBER: US/10/301,260A
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 09/520,822
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-301-260A-1

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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9
DB 349 ICWGNOLFFV 357
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; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1120
; CURRENT APPLICATION NUMBER: US/09/991,053
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-09-991-053-3

Query Match          83.6%; Score 46; DB 12; Length 568;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9
DB 384 VCHNOLFFV 392

RESULT 8
US-10-301-260A-3
; Sequence 3, Application US/10301260A
; Publication No. US20030118609A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen
; APPLICANT: Chen, Xiaojiang
; TITLE OF INVENTION: Vaccine compositions and methods for human papilloma
; FILE REFERENCE: Harvard/Harrison 12687/1123
; CURRENT APPLICATION NUMBER: US/10/301,260A
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 09/520,822
; PRIOR FILING DATE: 2000-03-18
; PRIOR APPLICATION NUMBER: 60/125208
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/148544
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Human papillomavirus type 18
US-10-301-260A-3

Query Match          83.6%; Score 46; DB 15; Length 568;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9
DB 384 VCHNOLFFV 392

RESULT 9
US-09-134-377-2
; Sequence 2, Application US/09134377
; Patent No. US20020015710A1
; GENERAL INFORMATION:
; APPLICANT: SCHLEGEL, C. Richard
; APPLICANT: JENSON, A. Bennett
```

APPLICANT: GHIM, Shin-Je  
TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,377  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/724,281  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Teakin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 010091-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-134-377-2

Query Match 78.2%; Score 43; DB 10; Length 503;  
Best Local Similarity 77.8%; Pred. No. 17;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ICWGNOLFV 9  
Db 325 IAWGNOLF 333

RESULT 10  
US-09-822-662-2  
Sequence 2, Application US/09822662  
Publication No. US20020197264A1  
GENERAL INFORMATION:  
APPLICANT: SCHLEGEL, C. Richard  
GHIM, Shin-Je  
Bennett  
TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/822,662  
FILING DATE: 02-Apr-2001  
CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/724,281  
FILING DATE: 08/24/2001  
ATTORNEY/AGENT INFORMATION:  
NAME: Teakin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 010091-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-822-662-2

Query Match 78.2%; Score 43; DB 11; Length 503;  
Best Local Similarity 77.8%; Pred. No. 17;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ICWGNOLFV 9  
Db 325 IAWGNOLF 333

RESULT 11  
US-10-149-846-2  
Sequence 2, Application US/10149846  
Publication No. US20030041345A1  
GENERAL INFORMATION:  
APPLICANT: Bayer Aktiengesellschaft  
TITLE OF INVENTION: Receptor-like protein kinases from plants  
FILE REFERENCE: WO72214  
CURRENT APPLICATION NUMBER: US/10/149,846  
PRIOR FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: DE 199 61 519.5  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 794  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-10-149-846-2

Query Match 72.7%; Score 40; DB 15; Length 794;  
Best Local Similarity 71.4%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 CWGNOLF 8  
Db 293 CWGNOLF 299

RESULT 12  
US-09-764-891-4533  
Sequence 4533, Application US/09764891  
Publication No. US20030077808A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC006  
CURRENT APPLICATION NUMBER: US/09/764,891  
PRIOR FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10231  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4533  
LENGTH: 147

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-764-891-4533

Query Match 69.1%; Score 38; DB 12; Length 147;  
Best Local Similarity 83.3%; Pred. No. 40;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNO 6  
Db 17 ICWGNE 22

RESULT 13  
US-09-832-292-39  
Sequence 39, Application US/09832292  
Patent No. US20020177205A1  
GENERAL INFORMATION:  
APPLICANT: Ryzanov, Alexey  
TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND  
FILE REFERENCE: 601-1-098CIP  
CURRENT APPLICATION NUMBER: US/09/832,292  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 09/632,131  
PRIOR FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 39  
LENGTH: 1907  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-832-292-39

Query Match 69.1%; Score 38; DB 11; Length 1907;  
Best Local Similarity 71.4%; Pred. No. 3.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CWCNQLP 8  
Db 1599 CWCQKLF 1605

RESULT 14  
US-10-101-464A-937  
Sequence 937, Application US/10101464A  
Publication No. US20030046728A1  
GENERAL INFORMATION:  
APPLICANT: Strabala, Timothy  
APPLICANT: Nieuwenhuizen, Nicolaas  
APPLICANT: Higgins, Colleen M.  
TITLE OF INVENTION: Compositions Isolated from Plant Cells  
FILE REFERENCE: 11000.1020C2  
CURRENT APPLICATION NUMBER: US/10/101,464A  
PRIOR FILING DATE: 2002-03-18  
PRIOR APPLICATION NUMBER: 09/704,302  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 09/228,986  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/162,866  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: PCT/US00/00724  
PRIOR FILING DATE: 2000-01-11  
NUMBER OF SEQ ID NOS: 989  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 937  
LENGTH: 416  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-10-101-464A-937

Query Match 67.3%; Score 37; DB 15; Length 416;

Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CWCNQLP 8  
Db 296 CWCNEHP 302

RESULT 15  
US-10-156-761-10059  
Sequence 10059, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 10059  
LENGTH: 459  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-10059

Query Match 67.3%; Score 37; DB 15; Length 459;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ICWGNOLEFV 9  
Db 403 LCWGEQMSV 411

Search completed: July 17, 2003, 19:53:25  
Job time : 21 Secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 17, 2003, 19:42:32 ; Search time 69 Seconds  
(without alignments)  
17.381 Million cell updates/sec

Title: US-09-980-177a-12

Perfect score: 55

Sequence: 1 ICWGNQLFV 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
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17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	22	HPV type 16 L1 pro
2	55	100.0	20	11	Papilloma virus ty
3	55	100.0	20	23	ABP47258
4	55	100.0	46	14	AAK32070
5	55	100.0	497	21	AAV71464
6	55	100.0	499	21	AAV71465
7	55	100.0	500	18	AAW18631
8	55	100.0	500	18	AAW15113
9	55	100.0	500	18	AAW15112
10	55	100.0	500	18	AAW24582

11	55	100.0	500	21	AAV99975	Human papillomavir
12	55	100.0	500	21	AAV99976	Human papillomavir
13	55	100.0	500	21	AAV99977	HPV 6 L1 protein m
14	55	100.0	500	21	AAV99978	HPV 6 L1 protein m
15	55	100.0	500	21	AAV99979	HPV 6 L1 protein m
16	55	100.0	500	21	AAV99980	HPV 6 L1 protein m
17	55	100.0	500	22	AAV99981	Human papillomavir
18	55	100.0	500	22	AAV99982	Human papillomavir
19	55	100.0	501	18	AAW32080	Human HPV6 L1 prot
20	55	100.0	501	18	AAW32081	Human HPV6 L1 prot
21	55	100.0	501	18	AAW32082	Human HPV6 L1 prot
22	55	100.0	501	18	AAW15109	Human HPV6 L1 prot
23	55	100.0	501	18	AAW15110	Human HPV6 L1 prot
24	55	100.0	501	18	AAW15111	Human HPV6 L1 prot
25	55	100.0	501	18	AAW26116	HPV1 mutant L1 pr
26	55	100.0	501	18	AAW10644	HPV6 mutant L1 pr
27	55	100.0	501	18	AAW10645	HPV6 mutant L1 pr
28	55	100.0	501	21	AAV99981	HPV 6 L1 protein m
29	55	100.0	504	22	AAV99982	Human papillomavir
30	55	100.0	505	14	AAK38807	Bovine p
31	55	100.0	505	14	AAK38808	Human papillomavir
32	55	100.0	505	19	AAW63116	Human papillomavir
33	55	100.0	505	19	AAW54034	HPV16 L1 gene prot
34	55	100.0	505	19	AAW54073	HPV16 L1 gene prot
35	55	100.0	505	19	AAW53486	Human papillomavir
36	55	100.0	505	19	AAW53487	Human papillomavir
37	55	100.0	505	19	AAW39903	HPV6 L1 capsid pr
38	55	100.0	505	19	AAW44142	Human papillomavir
39	55	100.0	505	19	AAW44143	Human papillomavir
40	55	100.0	505	20	AAV08019	Human papilloma vi
41	55	100.0	505	20	AAW96747	Human papillomavir
42	55	100.0	505	20	AAW96748	Human papillomavir
43	55	100.0	505	21	AAV57720	Human papillomavir
44	55	100.0	505	21	AAV53579	HPV16 L1 protein -
45	55	100.0	505	21	AAV53580	HPV16 L1 protein.

#### ALIGNMENTS

RESULT 1  
AAB46284 standard; peptide; 9 AA.  
ID AAB46284:.\*  
AC AAB46284:.\*  
DT 04-APR-2001 (first entry)  
XX  
DE HPV type 16 L1 protein cytotoxic T-cell epitope SEQ ID NO 12.  
XX  
KW Cytotoxic T cell epitope; L1 protein; antigenic; vaccine; antiviral;  
KW antitumor; immune response; tumor.  
XX  
OS Human papillomavirus.  
XX  
PN DE19925199-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 01-JUN-1999; 99DE-1025199.  
XX  
PR 01-JUN-1999; 99DE-1025199.  
XX  
PA (MED1-) MEDIGENE AG.  
XX  
PI Nieland J, Jochemus I;  
XX  
DR WPI; 2001-072111/09.  
XX  
PT New T cell epitopes from the papilloma virus L1 protein, useful for  
PT detecting or inducing an immune response, e.g. in vaccines  
XX  
PS Claim 1; Page 16; 24pp; German.

XX This invention describes novel T-cell epitopes (A) of the human  
CC Papilloma virus L1 protein. The invention also describes (a) compounds  
CC (1) containing an (A) provided it is not a natural L1 protein or an  
CC exclusively N- or C-terminal deletion variant of natural L1; (b) nucleic  
CC acid (II) that encodes (II) or (I); (c) vector, particularly an expression  
CC vector, that contains (II); (d) cells that contain, and preferably  
CC present, (A); (e) complex of (A) or (I) with at least one additional  
CC molecule (III); in vitro detection of T cell activation by a compound  
CC containing at least one (A); (f) preparing cells of (d); and (g) test  
CC system for in vitro detection of T cells. The products of the invention  
CC have antiviral and antitumor activity. (A), also compounds or complexes  
CC containing it or nucleic acid or vectors encoding it, is used for  
CC detection of an immune response, particularly detecting L1-specific  
CC cytotoxic T cells or to determine the L1 protein-specific antigenicity of  
CC compounds and complexes that contain (A), and for inducing a protective  
CC immune response against papilloma virus and related tumors, particularly  
CC as vaccines.

SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

Matches 9; Conservative 0; Indels 0;

OY 1 ICMGNQLFV 9  
|||  
1 ICMGNQLFV 9

DB 1 ICMGNQLFV 9

RESULT 2  
AAR04981  
ID AAR04981 standard; protein; 20 AA.

XX AAR04981:

XX 03-OCT-1990 (first entry)

XX Papilloma virus type 16 L1 peptide no. 24.

XX Papilloma virus; PV type 16; immunoglobulin; L1; ELISA: cervical cancer.

XX Synthetic.

XX WO9004790-A.

XX 03-MAY-1990.

XX 30-OCT-1989; 89WO-S000612.

XX 28-OCT-1989; 89SE-0003870.

XX (MEDS-) MEDSCAND AB.

XX Dillner J, Dillner L;

XX WPI; 1990-164122/21.

XX Detecting papilloma virus infections - by identifying specific  
XX antibodies against partic. viral proteins or fragments, esp. for  
XX rapid diagnosis of cervical cancer.

XX Claim 1; Page 30; 57pp; English.

XX The peptide is one of 66 overlapping peptides which together cover

XX the entire sequences of the L1 and L2 proteins of human PV type 16.

XX The peptide was found to be reactive with Ig Abs in the sera of

XX patients with type 16 cervical cancer. It can therefore be used in

XX immunoassays for the diagnosis of PV-associated neoplasia, esp.

XX carcinoma of the cervix uteri, and to assess the risk of development  
XX of such a carcinoma.  
XX See also AAR04958-R05023.

SQ Sequence 20 AA;

Query Match 100.0%; Score 55; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0074; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

OY 1 ICMGNQLFV 9  
|||  
3 ICMGNQLFV 11

DB 3 ICMGNQLFV 11

RESULT 3  
ABP47258

ID ABP47258 standard; Peptide; 20 AA.

XX ABP47258;

XX 15-AUG-2002 (first entry)

XX HPV16 L1 T-cell epitope peptide P30 SEQ ID NO 30.

XX HPV; human papillomavirus; T-cell epitope; L1; E7; virucide; cytostatic;

XX vaccine; immune response.

XX Human Papillomavirus 16.

XX WO200244384-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-EP14037.

XX 01-DEC-2000; 2000DE-1059631.

XX (MED1-) MEDIGENE AG.

XX Nieland J, Kaufmann A;

XX WPI; 2002-471833/50.

XX New T cell epitopes derived from human papilloma virus, useful for  
XX detecting immune activation and in a vaccine against papilloma virus

XX Example 1; Page 36; 126pp; German.

XX The invention relates to T-cell epitopes (I) derived from human  
XX papillomavirus (HPV). (I) have virucide and cytostatic activity and are  
XX able to induce a cytotoxic T cell response or mediate T helper cell  
XX function. (I) and also compounds (II) containing them, vectors that  
XX express (I) or (II), cells that contain (I) or (II) and/or complexes  
XX of (I) or (II) with another compound, are used to detect or induce an  
XX immune response, for diagnosis or therapy, particularly in vaccines for  
XX control of human papilloma virus infection. The present sequence is that  
XX of a HPV T-cell epitope of the invention.

SQ Sequence 20 AA;

Query Match 100.0%; Score 55; DB 23; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0074; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

OY 1 ICMGNQLFV 9  
|||  
4 ICMGNQLFV 12

DB 4 ICMGNQLFV 12

RESULT 4

ID AAR32070 standard; Protein; 46 AA.

XX AAR32070;

XX 07-JUN-1993 (first entry)



XX VLP reactive HPV16 L1 epitope 340-385.  
 DE B; epitope: human; Papilloma; virus; HPV-16; L1; antisera; ELISA; AI;  
 XX antigenic index; flexibility; accessibility; hydrophilicity; mice;  
 KM immunise; HPV16 capsid; papilloma virus like particle; VLP; diagnosis;  
 XX vaccine.  
 XX Synthetic.  
 OS  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 24..28  
 /note= "Epitope 363-367"  
 XX  
 PN MO9302184-A.  
 XX  
 XX 04-FEB-1993.  
 XX  
 PF 20-JUL-1992; 92WO-AU00364.  
 XX  
 PR 19-JUL-1991; 91AU-0007322.  
 XX  
 PA (CLSC-) CLS LTD.  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX  
 PI Frazer I, Zhou J;  
 XX  
 DR WPI; 1993-058783/07.  
 XX  
 PT Prodn. of papilloma virus-like particles - which contain L1 and  
 PT L2 proteins, useful as vaccine against papilloma virus infections  
 PT and in diagnosis  
 XX  
 PS Claim 39; Table 1; 63pp; English.  
 XX  
 CC The sequences given in AAR32054-73 are B epitopes which are derived  
 CC from the human papilloma virus-16 (HPV-16) L1 protein. These  
 CC epitopes were isolated by screening antisera from immunised animals  
 CC against a set of overlapping HPV-16 L1 peptides by ELISA. Possible  
 CC antigenic regions were identified using an antigenic index (AI) on the  
 CC basis of chain flexibility, high accessibility and a high degree of  
 CC hydrophilicity. A region with an AI value of over 1.5 was regarded as  
 CC a predicted B epitope. Five regions identified in this manner were  
 CC found to be within the 22 peptides to which major reactivity was  
 CC seen with antisera from mice immunised with synthetic HPV16 capsids.  
 CC These epitopes can be used to in the production of papilloma virus  
 CC like particles (VLPs) for use as diagnostic agents and as components  
 CC of vaccines for use with papilloma virus infections.  
 CC  
 SQ Sequence 46 AA;  
 Query Match 100.0%; Score 55; DB 14; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ICWGNQLFV 9  
 |||||  
 |||||  
 Db 10 ICWGNQLFV 18  
 RESULT 5  
 ID AAY71464 standard; Protein; 497 AA.  
 XX  
 AC AAY71464;  
 XX  
 DT 04-OCT-2000 (first entry)  
 XX  
 DE Chimeric biotin-binding human papillomavirus mutant L1 protein-168.  
 KM Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;  
 KM cytosolic; antiviral; gene therapy; vaccine; capsomere; VLP;  
 KM virus-like particle; viral antigen; tumour; cyclooxin; cytokine; IL;

KM interleukin; chemotherapeutic agent; radioactive agent; mutant; mutein.  
 XX  
 OS Chimeric - Human papillomavirus 16.  
 OS Chimeric - Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..483  
 FT Binding-site /label= HPV\_16\_mutant\_L1\_protein  
 FT /label= 484..497  
 FT Region /label= Biotin\_binding\_peptide  
 FT /note= "(Gly)3 hinge"  
 XX  
 PN MO200031128-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 22-NOV-1999; 99WO-US27555.  
 XX  
 PR 23-NOV-1998; 98US-0109510.  
 PR 06-OCT-1999; 99US-0413611.  
 XX  
 PA (LOYO ) UNIV LOYOLA CHICAGO.  
 XX  
 PI Mueller M, Kaest WM, Nieland JD, Velders MP;  
 XX  
 DR WPI; 2000-400041/34.  
 DR N-PSDB; AAD01237.  
 XX  
 PT Chimeric protein comprising a papillomavirus L1 or L2 protein and a  
 PT biotin-binding polypeptide, useful for delivering substances such as  
 PT proteins, nucleic acids and lipids into cells, particularly  
 PT papillomavirus infected cells  
 XX  
 PS Example 1; Page 18-20; 27pp; English.  
 XX  
 CC The patent discloses a chimeric protein comprising papillomavirus L1 or  
 CC L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus  
 CC or virus-like particle (VLP) comprising the chimeric protein is used  
 CC for delivering a wide variety of biotinylated compounds e.g. proteins,  
 CC nucleic acids and lipids into cells, particularly papillomavirus infected  
 CC cells. The chimeric protein may also be used as a vaccine when the  
 CC biotinylated substance is a viral antigen e.g. papillomavirus E2 or E7  
 CC proteins. It may be useful for treating tumours or other papillomavirus-  
 CC related lesions when the substance is a cyclooxin, chemotherapeutic  
 CC agent, radioactive agent, or a gene encoding a cytokine or interleukin.  
 CC The present sequence is a chimeric protein 168 consisting  
 CC of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotin-  
 CC binding peptide at the C-terminus. The L1 protein was derived from  
 CC the wild-type sequence by deleting the amino acid Cys428. The  
 CC modification was done to prevent assembly of VLPs while allowing the  
 CC production of capsomeres at high efficiencies.  
 CC  
 SQ Sequence 497 AA;  
 Query Match 100.0%; Score 55; DB 21; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ICWGNQLFV 9  
 |||||  
 |||||  
 Db 323 ICWGNQLFV 331  
 RESULT 6  
 ID AAY71465 standard; Protein; 499 AA.  
 XX  
 AC AAY71465;  
 XX  
 DT 04-OCT-2000 (first entry)  
 XX  
 DE Chimeric biotin-binding human papillomavirus mutant L1 protein-169.

XX	Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;
KM	Cytosolic; antiviral; gene therapy; vaccine; capsomere; VLP;
KM	virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL;
KM	interleukin; chemotherapeutic agent; radioactive agent; mutant; mutein.
OS	Chimeric - Human papillomavirus 16.
OS	Chimeric - Unidentified.
XX	
FE	Key
FT	Region
FT	Binding-site
FT	Region
FT	/label= Biotin_binding_domain
FT	484..486
FT	/note= "(Gly) 3 hinge"
XX	
PN	W0200031128-A1.
PD	02-JUN-2000.
PF	22-NOV-1999; 99WO-US27555.
PR	23-NOV-1998; 98US-0109510.
PR	06-OCT-1999; 99US-0413611.
PA	(LOYO ) UNIV LOYOLA CHICAGO.
P1	Mueller M, Kast WM, Nieland JD, Velders MP;
DR	WPI: 2000-400041/34.
DR	N-PDB; AAD01238.
XX	
PT	Chimeric protein comprising a papillomavirus L1 or L2 protein and a
PT	biotin-binding polypeptide, useful for delivering substances such as
P3	proteins, nucleic acids and lipids into cells, particularly
P3	papillomavirus infected cells -1
XX	
P3	Example 1, Page 23-24; 27pp; English.
XX	
CC	The patent discloses a chimeric protein comprising papillomavirus L1 or
CC	L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus
CC	or virus-like particle (VLP) comprising the chimeric protein is used
CC	for delivering a wide variety of bioconjugated compounds e.g. proteins,
CC	nucleic acids and lipid into cells, particularly papillomavirus infected
CC	cells. The chimeric protein may also be used as a vaccine when the
CC	bioconjugated substance is a viral antigen e.g. papillomavirus E2 or E7
CC	proteins. It may be useful for treating tumours or other papillomavirus-
CC	related lesions when the substance is a cytotoxic, chemotherapeutic
CC	agent, radioactive agent, or a gene encoding a cytokine or interleukin.
CC	The present sequence is a chimeric protein 169 consisting
CC	of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotin-
CC	binding peptide at the C-terminus. The L1 protein was derived from
CC	the wild-type sequence by deleting the amino acid Cys428. The
CC	modification was done to prevent assembly of VLPs while allowing the
CC	production of capsomeres at high efficiencies.
XX	
SQ	Sequence 499 AA:
QY	Query Match 100.0%; Score 55; DB 21; Length 499;
DB	Best Local Similarity 100.0%; Fred. No. 0.18;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
	1 ICMGNOLFV 9
	323 ICMGNOLFV 331
RESULT 7	
ID	AAW18631 standard; protein; 500 AA.
XX	AAW18631;
AC	

```

XX 30-JAN-1998 (first entry)
XX
XX Human HPV6 L1 protein (wild-type).
XX
XX Human papillomavirus 11; HPV11; L1 protein; late gene 1;
XX virus capsid protein; non-malignant condylomata;
XX genital wart; laryngeal papilloma; HPV6; virus-like particle; VLP;
XX vaccine; epitope; neutralising antibodies; immunity.
XX
XX Human papillomavirus.
XX
XX WO9718301-A1.
XX
XX 22-MAY-1997.
XX
XX 12-NOV-1996; 96WO-US18322.
XX
XX 07-MAR-1996; 96GB-0004812.
XX PR 15-NOV-1995; 95US-0006788.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Benincasa D, Ludmerer S, Mark GE;
XX WPI, 1997-289277/26.
XX
XX Synthetic virus-like particles from human papillomavirus type 6 and
XX PT 11 mutant constructs - useful for characterising recombinant
XX PT virus-like particles, e.g. manufactured HPV11 VLPs for use in
XX PT vaccines
XX
XX PS Claim 1; Fig 1; 33pp: English.
XX
XX This is the amino acid sequence of human papillomavirus 6 (HPV6)
XX corresponding to the L1 protein (late gene 1 coding for virus capsid
XX proteins). HPV6 is a causative agent of non-malignant condylomata of
XX genital or respiratory mucosa (genital warts) and laryngeal papilloma
XX and is structurally similar to the HPV11 amino acid sequence. Virus-like
XX particles (VLP's) can be generated from recombinant HPV6 and HPV11 which
XX are useful in characterising human papillomavirus infection. Due to the
XX structural similarity of HPV6 and HPV11, HPV6 derivative VLPs can be used
XX in an assay to characterise recombinant HPV11 VLPs in order to verify
XX that manufactured HPV11 VLPs, e.g. a HPV11 vaccine, contain the epitope
XX for neutralisation by antibodies. This will allow the large scale
XX production of papillomavirus proteins with the immunity-conferring
XX properties of native proteins.
XX
XX
XX SQ Sequence 500 AA;
XX
XX Query Match 100.0%; Score 55; DB 18; Length 500;
XX Best Local Similarity 100.0%; Pred. No. 0.18;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 ICWGNQLFV 9
XX |||||
XX 319 ICWGNQLFV 327
XX
XX RESULT 8
XX AAM15113
XX ID AAM15113 standard; protein; 500 AA.
XX
XX AC AAM15113;
XX
XX DT 02-FEB-1998 (first entry)
XX
XX DE Human HPV6 L1 protein construct HPV6:4 (variant 2).
XX
XX Human papillomavirus 11; HPV11; L1 protein; late gene 1;
XX virus capsid protein; non-malignant condylomata;
XX genital wart; laryngeal papilloma; HPV6; virus-like particle; VLP;
XX vaccine; epitope; neutralising antibodies; immunity; mutant.

```

```

XX OS Synthetic.
XX OS Human papillomavirus.
XX FH Key
XX FT Misc-difference 131
XX FT /label= S131G
XX FT /note= "Wild-type Ser is replaced by Gly."
XX PN MO9718301-A1.
XX PD 22-MAY-1997.
XX PF 12-NOV-1996; 96WO-US18322.
XX PR 07-MAR-1996; 96GB-0004812.
XX PR 15-NOV-1995; 95US-0006788.
XX PA (MERI ) MERCK & CO INC.
XX PI Benincasa D, Ludmerer S, Mark GE;
XX DR WPI; 1997-289277/26.
XX XX
XX PT Synthetic virus-like particles from human papillomavirus type 6 and
XX PT 11 mutant constructs - useful for characterising recombinant
XX PT virus-like particles, e.g. manufactured HPV11 VLPs for use in
XX PS vaccines
XX PS
XX PS Claim 1; Page -; 33pp; English.
XX CC This amino acid sequence represents a variant of the human
XX CC papillomavirus 6 (HPV6) corresponding to the L1 protein (late gene 1
XX CC coding for virus capsid proteins) and is used to generate a synthetic
XX CC virus-like particle (VLP). Altering the HPV6 L1 sequence at residue 131
XX CC facilitates binding by HPV11 specific neutralising monoclonal
XX CC antibodies. This sequence is a variant of the mutant HPV6:4 (see
XX CC AAM15109) and was generated by back-mutation in order to carry out
XX CC binding assays to determine the minimal epitope for binding neutralising
XX CC antibodies. HPV6 and HPV11 are causative agents of non-malignant
XX CC condylomata of genital or respiratory mucosa (genital warts) and
XX CC laryngeal papilloma and is structurally similar to the HPV11 amino acid
XX CC sequence. Virus-like particles can be generated from recombinant HPV6 and
XX CC HPV11 which are useful in characterising human papillomavirus infection.
XX CC Due to the structural similarity of HPV6 and HPV11, HPV6 derivative VLPs
XX CC can be used in an assay to characterise recombinant HPV11 VLPs in order
XX CC to verify that manufactured HPV11 VLPs, e.g. a HPV11 vaccine, contain the
XX CC epitope for neutralisation by antibodies. This will allow the large
XX CC scale production of papillomavirus proteins with the immunity-conferring
XX CC properties of native proteins.
XX CC Note: The present sequence does not appear in the specification; it
XX CC has been made by modifying the native HPV6 L1 protein sequence which
XX CC is provided in Figure 1.
XX XX
XX SQ Sequence 500 AA;
XX
XX Query Match 100.0%; Score 55; DB 18; Length 500;
XX Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;
XX
XX QY 1 ICWGNQJLFV 9
XX |||||
XX |||||
XX Db 319 ICWGNQJLFV 327
XX
XX RESULT 9
XX AAM15112
XX ID AAM15112 standard; protein; 500 AA.
XX XX
XX AC AAM15112;
XX XX
XX DT 02-FEB-1998 (first entry)
XX XX

```

```

DE DE Human HPV6 L1 protein construct HPV6:4 (variant 1).
XX XX
XX KW Human papillomavirus 11; HPV11; L1 protein; late gene 1;
XX KW virus capsid protein; causative agent; non-malignant condylomata;
XX KW genital wart; laryngeal papilloma; HPV6; virus-like particle; VLP;
XX KW vaccine; epitope; neutralising antibodies; immunity; mutant.
XX XX
XX OS Synthetic.
XX OS Human papillomavirus.
XX XX
XX FH Key
XX FT Misc-difference 131
XX FT /label= S131G
XX FT /note= "Wild-type Ser is replaced by Gly."
XX FT Misc-difference 245
XX FT /label= F245Y
XX FT /note= "Wild-type Phe is replaced by Tyr."
XX FT Misc-difference 277
XX FT /label= G277N
XX FT /note= "Wild-type Gly is replaced by Aen."
XX PN MO9718301-A1.
XX PD 22-MAY-1997.
XX PF 12-NOV-1996; 96WO-US18322.
XX PR 07-MAR-1996; 96GB-0004812.
XX PR 15-NOV-1995; 95US-0006788.
XX PA (MERI ) MERCK & CO INC.
XX PI Benincasa D, Ludmerer S, Mark GE;
XX DR WPI; 1997-289277/26.
XX XX
XX PT Synthetic virus-like particles from human papillomavirus type 6 and
XX PT 11 mutant constructs - useful for characterising recombinant
XX PT virus-like particles, e.g. manufactured HPV11 VLPs for use in
XX PS vaccines
XX PS
XX PS Claim 1; Page -; 33pp; English.
XX CC This amino acid sequence represents a variant of the human
XX CC papillomavirus 6 (HPV6) corresponding to the L1 protein (late gene 1
XX CC coding for virus capsid proteins) and is used to generate a synthetic
XX CC virus-like particle (VLP). By altering the HPV6 L1 sequence at residues
XX CC 131, 245 and 277 the sequence resembles that of the HPV11 L1 sequence
XX CC and facilitates binding by HPV11 specific neutralising monoclonal
XX CC antibodies. This sequence is a variant of the mutant HPV6:4 (see
XX CC AAM15109) and was generated by back-mutation in order to carry out
XX CC binding assays to determine the minimal epitope for binding neutralising
XX CC antibodies. HPV6 and HPV11 are causative agents of non-malignant
XX CC condylomata of genital or respiratory mucosa (genital warts) and
XX CC laryngeal papilloma and is structurally similar to the HPV11 amino acid
XX CC sequence. Virus-like particles (VLP's) can be generated from recombinant
XX CC HPV6 and HPV11 which are useful in characterising human papillomavirus
XX CC infection. Due to the structural similarity of HPV6 and HPV11, HPV6
XX CC derivative VLPs can be used in an assay to characterise recombinant HPV11
XX CC VLPs in order to verify that manufactured HPV11 VLPs, e.g. a HPV11
XX CC vaccine, contain the epitope for neutralisation by antibodies. This will
XX CC allow the large scale production of papillomavirus proteins with the
XX CC immunity-conferring properties of native proteins.
XX CC Note: The present sequence does not appear in the specification; it
XX CC has been made by modifying the native HPV6 L1 protein sequence which
XX CC is provided in Figure 1.
XX XX
XX SQ Sequence 500 AA;
XX
XX Query Match 100.0%; Score 55; DB 18; Length 500;
XX Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;

```

QY 1 ICMGNOL.FV 9  
 ID |||||  
 DB 319 ICMGNOL.FV 327

## RESULT 10

AAW24582  
 ID AAW24582 standard; protein; 500 AA.

AAW24582;  
 12-NOV-1997 (first entry)

HPV6 L1 protein.

L1 protein; HPV; human papillomavirus; HPV6; HPV11; virus-like particle; normalizing condyloma; respiratory mucosa; laryngeal papillomas; neutralising antibody; major capsid protein; vaccine; therapy.

Human papillomavirus.

WO9704076-A1.

06-FEB-1997.

15-JUL-1996; 96WO-US11739.

22-FEB-1996; 96GB-0003758.

19-JUL-1995; 95US-0001504.

(MERI) MERCK & CO INC.

Benincasa D, Hollis GF, Ludmerer S, Mark GE;

WPI; 1997-132620/12.

Synthetic virus like particles based on human papilloma virus 6 and 11 mutants - used to characterise recombinant HPV11 particles,

intended for vaccines, to ensure presence of neutralising epitope

Disclosure; Fig 3; 29pp; English.

This sequence represents the human papillomavirus (HPV) 6 L1 protein. Mutations of this sequence, and of the HPV11 L1 protein sequence (see AAW24581), are used in the synthetic virus-like particles (VLP) of the invention. In humans, HPV cause distinct diseases. HPV6, and HPV11 are among the HPV strains that cause nonmalignant condylomata of the genital or respiratory mucosa. HPV6 and HPV11 are the causative agents for more than 90% of all condyloma and laryngeal papillomas. The production of neutralising antibodies (Ab) to papillomavirus antigens prevents infection with the homologous virus. The L1 protein is the major capsid protein of HPV. It is thought that the L2 protein is internal to the L1 protein. The L1 open reading frame is highly conserved among different papillomaviruses. The specified HPV11 mutants have lost the ability to generate neutralising Ab. The HPV6 VLP contain the neutralising epitope of HPV11, and are used to confirm that a batch of HPV11 VLP, intended for vaccine use, retains the neutralising epitope. The HPV6 VLP can also be used to test whether polyclonal antisera raised against HPV11 VLP, or human samples, have neutralising activity. They may also be used to raise Ab against the HPV11 neutralising epitope.

Sequence 500 AA;

Query Match 100.0%; Score 55; DB 18; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 ICMGNOL.FV 9  
 ID |||||  
 DB 319 ICMGNOL.FV 327

## RESULT 11

AAV99975  
 ID AAV99975 standard; protein; 500 AA.

AAV99975;

07-NOV-2000 (first entry)

Human papillomavirus 6 L1 protein mutant PA9Y/R53K.

HPV6; HPV11; mutant; mutein; antiviral; vaccine; L1 protein.

Human papillomavirus.

Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 49 /note= "wild-type phe substituted by Tyr"  
 FT /note= 53  
 FT Misc-difference 53 /note= "wild-type Arg substituted by Lys"

WO200035479-A1.

22-JUN-2000.

14-DEC-1999; 99WO-US29577.

17-DEC-1998; 98US-0112610.

(MERI) MERCK & CO INC.

Jansen KU, Ling JC, Ludmerer SW, McClements WL, Wang X;

WPI; 2000-431502/37.

Recombinant papillomavirus L1 protein, useful in an assay for distinguishing between human papillomavirus (HPV) 6 and HPV11 antibodies, and in a vaccine

Example 4; Page -; 28pp; English.

The present invention relates to human papillomavirus (HPV) L1 protein mutants. The present sequence is the HPV 6 L1 protein containing a substitution mutation. The mutants were created to define the amino acid residues that confer antigenic type-specificity on HPV subtypes 6 and 11. The mutants may be used in an assay to distinguish between the presence of HPV6 and HPV11 antibodies in a sample. The mutant proteins can also be used in vaccines. This assay overcomes the failure of previous assays to distinguish the high identity between HPV6 and HPV 11.  
 Note: The present sequence is not shown in the specification but is derived from the HPV wild type L1 protein.

Sequence 500 AA;

Query Match 100.0%; Score 55; DB 21; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 ICMGNOL.FV 9  
 ID |||||  
 DB 319 ICMGNOL.FV 327

## RESULT 12

AAV99976  
 ID AAV99976 standard; protein; 500 AA.

AAV99976;

07-NOV-2000 (first entry)

Human papillomavirus 6 L1 protein mutant T345S/T346K/S348A.

XX	HPV6; HPV11; mutant; mutein; antiviral; vaccine; L1 protein.	
XX	Human papillomavirus.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
XX	Misc-difference 345	/note= "Wild-type Thr substituted by Ser"
XX	Misc-difference 346	/note= "Wild-type Thr substituted by Lys"
XX	Misc-difference 348	/note= "Wild-type Ser substituted by Ala"
XX	WO200035479-A1.	
XX	22-JUN-2000.	
XX	14-DEC-1999;	99WO-US29577.
XX	17-DEC-1998;	98US-0112610.
XX	(MERI ) MERCK & CO INC.	
XX	Jansen KU, Ling JC, Ludmerer SW, McClements WL, Wang X;	
XX	WPI; 2000-431502/37.	
XX	Recombinant papillomavirus L1 protein, useful in an assay for	
XX	distinguishing between human papillomavirus (HPV) 6 and HPV11	
XX	antibodies, and in a vaccine	
XX	Claim 6; Page -; 28pp; English.	
XX	The present invention relates to human papillomavirus (HPV) L1 protein	
XX	mutants. The present sequence is the HPV 6 L1 protein containing a	
XX	substitution mutation. The mutants were created to define the amino acid	
XX	residues that confer antigenic type-specificity on HPV subtypes 6 and	
XX	11. The mutants may be used in an assay to distinguish between the	
XX	presence of HPV6 and HPV11 antibodies in a sample. The mutant proteins	
XX	can also be used in vaccines. This assay overcomes the failure of	
XX	previous assays to distinguish the high identity between HPV6 and HPV	
XX	11.	
XX	Note: The present sequence is not shown in the specification but is	
XX	derived from the HPV wild type L1 protein.	
XX	Sequence 500 AA;	
XX		
XX	Query Match	100.0%; Score 55; DB 21; Length 500;
XX	Best Local Similarity	100.0%; Pred. No. 0.18;
XX	Matches 9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX		
XX	1 ICMGNQLFV 9	
XX		
XX	319 ICMGNQLFV 327	
XX		
XX	RESULT 13	
XX	AA999977	
XX	AA999977 standard; protein; 500 AA.	
XX	AA999977;	
XX	07-NOV-2000 (first entry)	
XX	HPV 6 L1 protein mutant E262T/T270D/S276G/G277N/T280S/G283A/N289H.	
XX	HPV6; HPV11; mutant; mutein; antiviral; vaccine; L1 protein.	
XX	Human papillomavirus.	
XX	Synthetic.	
XX		
XX	Key	Location/Qualifiers
XX	Misc-difference 262	

FT	Misc-difference	270	/note= "Wild-type Glu substituted by Thr"
FT	Misc-difference	276	/note= "Wild-type Thr substituted by Asp"
FT	Misc-difference	276	/note= "Wild-type Ser substituted by Gly"
FT	Misc-difference	277	/note= "Wild-type Gly substituted by Asn"
FT	Misc-difference	280	/note= "Wild-type Thr substituted by Ser"
FT	Misc-difference	283	/note= "Wild-type Gly substituted by Ala"
FT	Misc-difference	289	/note= "Wild-type Asn substituted by His"
XX			
PN	WO200035479-A1.		
XX			
PD	22-JUN-2000.		
XX			
PP	14-DEC-1999; 99WO-US29577.		
XX			
PR	17-DEC-1998; 98US-0112610.		
XX			
PA	(MERI ) MERCK & CO INC.		
XX			
PI	Jansen KU, Ling JC, Ludmerer SM, McClements WL, Wang X;		
DR	WPI; 2000-431502/37.		
XX			
PT	Recombinant papillomavirus L1 protein, useful in an assay for		
PT	distinguishing between human papillomavirus (HPV) 6 and HPV11		
PT	antibodies, and in a vaccine -		
XX			
PS	Claim 6; Page -; 28pg; English.		
XX			
CC	The present invention relates to human papillomavirus (HPV) L1 protein		
CC	mutants. The present sequence is the HPV 6 L1 protein containing a		
CC	substitution mutation. The mutants were created to define the amino acid		
CC	residues that confer antigenic type-specificity on HPV subtypes 6 and		
CC	11. The mutants may be used in an assay to distinguish between the		
CC	presence of HPV6 and HPV11 antibodies in a sample. The mutant proteins		
CC	can also be used in vaccines. This assay overcomes the failure of		
CC	previous assays to distinguish the high identity between HPV6 and HPV		
CC	11.		
CC	Note: The present sequence is not shown in the specification but is		
CC	derived from the HPV wild type L1 protein.		
SO	Sequence 500 AA;		
XX			
QY	1 ICWGNOLEFV 9		
Db	319 ICWGNOLEFV 327		
Query Match	100.0%;	Score 55;	DB 21; Length 500;
Best Local Similarity	100.0%;	Pred. No. 0.18;	
Matches	9;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
RESULT 14			
AAI99978			
ID	AAI99978 standard; protein; 500 AA.		
XX			
AC	AAI99978;		
XX			
DT	07-NOV-2000 (first entry)		
DE	HPV 6 L1 protein mutant P49Y/R53K/A54V/K169T/T172S/P175S/A178N.		
XX			
KW	HPV6; HPV11; mutanc; mutcin; antiviral; vaccine; L1 protein.		
XX			
OS	Human papillomavirus.		
XX			
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	

```

FT Misc-difference 49 /note= "Wild-type Phe substituted by Tyr"
FT Misc-difference 53 /note= "Wild-type Arg substituted by Lys"
FT Misc-difference 54 /note= "Wild-type Ala substituted by Val"
FT Misc-difference 169 /note= "Wild-type Lys substituted by Thr"
FT Misc-difference 172 /note= "Wild-type Thr substituted by Ser"
FT Misc-difference 175 /note= "Wild-type Pro substituted by Ser"
FT Misc-difference 178 /note= "Wild-type Ala substituted by Asn"
FT WO200035479-A1.
XX
XX
XX 22-JUN-2000.
XX
XX 14-DEC-1999; 99WO-US29577.
XX
XX 17-DEC-1998; 98US-0112610.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Jansen KU, Ling JC, Ludmerer SW, McClements WL, Wang X;
XX WPI, 2000-431502/37.
XX
XX Recombinant papillomavirus L1 protein, useful in an assay for
XX distinguishing between human papillomavirus (HPV) 6 and HPV11
XX antibodies, and in a vaccine
XX
XX Example 8; Page -: 28pp; English.
XX
XX The present invention relates to human papillomavirus (HPV) L1 protein
XX mutants. The present sequence is the HPV 6 L1 protein containing a
XX substitution mutation. The mutants were created to define the amino acid
XX residues that confer antigenic type-specificity on HPV subtypes 6 and
XX 11. The mutants may be used in an assay to distinguish between the
XX presence of HPV6 and HPV11 antibodies in a sample. The mutant proteins
XX can also be used in vaccines. This assay overcomes the failure of
XX previous assays to distinguish the high identity between HPV6 and HPV
XX 11.
XX Note: The present sequence is not shown in the specification but is
XX derived from the HPV wild type L1 protein.
XX
XX Sequence 500 AA;
SQ
Query Match 100.0%; Score 55; DB 21; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ICWGNOQLFV 9
DB 319 ICWGNOQLFV 327

```

RESULT 15  
AA999979  
ID AA999979 standard; protein; 500 AA.  
XX  
XX AA999979;  
DT 07-NOV-2000 (first entry)  
XX  
XX HPV 6 L1 protein mutant K169T/R172S/P175S/A178N.  
XX  
XX HPV6; HPV11; mutant; mutein; antiviral; vaccine; L1 protein.  
OS Human papillomavirus.  
QS Synthetic.  
XX

```

FH Key Location/Qualifiers
FT Misc-difference 169 /note= "Wild-type Lys substituted by Thr"
FT Misc-difference 172 /note= "Wild-type Thr substituted by Ser"
FT Misc-difference 175 /note= "Wild-type Pro substituted by Ser"
FT Misc-difference 178 /note= "Wild-type Ala substituted by Asn"
FT WO200035479-A1.
XX
XX
XX 22-JUN-2000.
XX
XX 14-DEC-1999; 99WO-US29577.
XX
XX 17-DEC-1998; 98US-0112610.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Jansen KU, Ling JC, Ludmerer SW, McClements WL, Wang X;
XX WPI, 2000-431502/37.
XX
XX Recombinant papillomavirus L1 protein, useful in an assay for
XX distinguishing between human papillomavirus (HPV) 6 and HPV11
XX antibodies, and in a vaccine
XX
XX Claim 6; Page -: 28pp; English.
XX
XX The present invention relates to human papillomavirus (HPV) L1 protein
XX mutants. The present sequence is the HPV 6 L1 protein containing a
XX substitution mutation. The mutants were created to define the amino acid
XX residues that confer antigenic type-specificity on HPV subtypes 6 and
XX 11. The mutants may be used in an assay to distinguish between the
XX presence of HPV6 and HPV11 antibodies in a sample. The mutant proteins
XX can also be used in vaccines. This assay overcomes the failure of
XX previous assays to distinguish the high identity between HPV6 and HPV
XX 11.
XX Note: The present sequence is not shown in the specification but is
XX derived from the HPV wild type L1 protein.
XX
XX Sequence 500 AA;
SQ
Query Match 100.0%; Score 55; DB 21; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ICWGNOQLFV 9
DB 319 ICWGNOQLFV 327

```

Search completed: July 17, 2003, 19:44:21  
Job time : 70 secs

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## OM protein - protein search, using sw model

Run on: July 17, 2003, 19:42:36 ; Search time 14 Seconds  
(without alignments)  
18.915 Million cell updates/sec

Title: US-09-980-177a-12

Perfect score: 55

Sequence: 1 ICWGNQLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	20	1	US-07-678-974D-24
2	55	100.0	20	2	US-08-945-168-29
3	55	100.0	497	4	US-09-413-611A-6
4	55	100.0	499	4	US-09-413-611A-8
5	55	100.0	500	2	US-08-987-519-2
6	55	100.0	505	4	US-08-944-368A-2
7	55	100.0	505	4	US-09-820-764-2
8	55	100.0	532	3	US-08-737-336-6
9	50	90.9	500	2	US-08-987-519-1
10	49	89.1	501	2	US-08-987-519-3
11	47	85.5	507	2	US-08-409-122-2
12	47	85.5	507	2	US-08-408-669-2
13	43	78.2	503	2	US-08-724-811-2
14	35	63.6	322	2	US-08-622-354-3
15	34	61.8	508	2	US-08-724-281-1
16	33	60.0	37	1	US-08-212-236-10
17	33	60.0	40	1	US-08-033-873-10
18	33	60.0	40	2	US-08-356-832-10
19	33	60.0	40	4	US-08-988-703-10
20	33	60.0	58	1	US-08-566-800A-34
21	33	60.0	58	1	US-08-566-800A-50
22	33	60.0	58	2	US-08-398-010A-49
23	33	60.0	58	2	US-08-398-010A-65
24	33	60.0	58	2	US-08-398-628A-49
25	33	60.0	58	2	US-08-398-628A-65
26	33	60.0	58	2	US-08-932-589-34
27	33	60.0	58	2	US-08-932-589-50

28	33	60.0	58	2	US-08-399-115A-49	Sequence 49, Appl
29	33	60.0	58	2	US-08-399-115A-65	Sequence 65, Appl
30	33	60.0	332	4	US-09-172-952-23	Sequence 23, Appl
31	33	60.0	352	4	US-09-413-814-24	Sequence 24, Appl
32	33	60.0	366	4	US-09-134-001C-4799	Sequence 4799, Ap
33	33	60.0	393	4	US-09-629-616-2	Sequence 2, Appl1
34	32	58.2	20	1	US-08-416-950-7	Sequence 7, Appl1
35	32	58.2	20	1	US-08-464-235-18	Sequence 18, Appl1
36	32	58.2	20	2	US-08-468-830-7	Sequence 35, Appl1
37	32	58.2	20	2	US-08-469-830-7	Sequence 7, Appl1
38	32	58.2	20	4	US-08-463-486-18	Sequence 18, Appl1
39	32	58.2	20	4	US-08-464-496-11	Sequence 11, Appl1
40	32	58.2	20	4	US-08-197-484-101	Sequence 101, App
41	32	58.2	20	4	US-09-556-877-156	Sequence 156, App
42	32	58.2	20	4	US-09-620-412C-156	Sequence 156, App
43	32	58.2	20	5	PCT-US92-07218-11	Sequence 11, Appl1
44	32	58.2	20	5	PCT-US94-02195-18	Sequence 18, Appl1
45	32	58.2	20	5	PCT-US95-02121-101	Sequence 101, App

## ALIGNMENTS

RESULT 1  
US-07-678-974D-24  
; Sequence 24, Application US/07678974D  
; Patent No. 5629146  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; APPLICANT: DILLNER, LENA  
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERMAN & AISENBERG  
; STREET: 1730 RHODE ISLAND AVENUE, N.W.,  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-3186  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/678,974D  
; FILING DATE: 25-JUN-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: AISENBERG, Irwin M.  
; REGISTRATION NUMBER: 19,007  
; REFERENCE/DOCKET NUMBER: SG19171  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-293-1404  
; TELEFAX: 202-872-0493  
; TELEX: 440 069 AIS UI  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-07-678-974D-24

Query Match 100.0%; Score 55; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 3 ICWGNQLFV 11

RESULT 2  
US-08-945-168-29  
; Sequence 29, Application US/08945168  
; Patent No. 5989548  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA  
; TITLE OF INVENTION: VTRUS  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,168  
; FILING DATE: 18-DEC-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE96/00533  
; FILING DATE: 23-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9501512-9  
; FILING DATE: 24-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-945-168-29  
Query Match 100.0%; Score 55; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||  
Db 3 ICWGNQLFV 11

RESULT 3  
US-09-413-611A-6  
; Sequence 6, Application US/09413611A  
; Patent No. 6380364  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Martin  
; APPLICANT: Kast, Wilbe  
; APPLICANT: Nieland, John  
; APPLICANT: Veldeers, Markwin  
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein  
; FILE REFERENCE: 202325  
; CURRENT APPLICATION NUMBER: US/09/413,611A  
; CURRENT FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: US 60/109,510  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: biotin-binding  
US-09-413-611A-6  
Query Match 100.0%; Score 55; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 0.072;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||  
Db 323 ICWGNQLFV 331

RESULT 4  
US-09-413-611A-8  
; Sequence 8, Application US/09413611A  
; Patent No. 6380364  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Martin  
; APPLICANT: Kast, Wilbe  
; APPLICANT: Nieland, John  
; APPLICANT: Veldeers, Markwin  
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein  
; FILE REFERENCE: 202325  
; CURRENT APPLICATION NUMBER: US/09/413,611A  
; CURRENT FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: US 60/109,510  
; PRIOR FILING DATE: 1998-11-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: biotin-binding  
US-09-413-611A-8  
Query Match 100.0%; Score 55; DB 4; Length 499;  
Best Local Similarity 100.0%; Pred. No. 0.072;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||  
Db 323 ICWGNQLFV 331

RESULT 5  
US-08-987-519-2  
; Sequence 2, Application US/08987519  
; Patent No. 5952216  
; GENERAL INFORMATION:  
; APPLICANT: Ludmerer, Steven  
; TITLE OF INVENTION: SYNTHETIC HPV16 VIRUS-LIKE PARTICLES  
; FILE REFERENCE: 19853  
; CURRENT APPLICATION NUMBER: US/08/987,519  
; CURRENT FILING DATE: 1997-12-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Human Papillomavirus  
US-08-987-519-2  
Query Match 100.0%; Score 55; DB 2; Length 500;



Best Local Similarity 100.0%; Pred. No. 0.072;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
| | | | |  
Db 319 ICWGNOLFV 327

## RESULT 6

US-08-944-368A-2  
; Sequence 2, Application US/08944368A  
; Patent No. 6228368  
; GENERAL INFORMATION:  
; APPLICANT: Gissman, et al.  
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine  
; TITLE OF INVENTION: Formulations and Methods of Use  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 233 South Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,368A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27013/34028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 505 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-944-368A-2

Query Match 100.0%; Score 55; DB 4; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
| | | | |  
Db 323 ICWGNOLFV 331

RESULT 7  
US-09-820-764-2  
; Sequence 2, Application US/09820764  
; Patent No. 6352696  
; GENERAL INFORMATION:  
; APPLICANT: BURGER, Alexander

; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
; FORMULATIONS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.

; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/820,764  
; FILING DATE: 30-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/026,896  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sandercock, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37067/102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 505 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 55; DB 4; Length 505;  
Best Local Similarity 100.0%; Pred. No. 0.073;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
| | | | |  
Db 323 ICWGNOLFV 331

RESULT 8  
US-08-737-336-6  
; Sequence 6, Application US/08737336  
; Patent No. 6013262  
; GENERAL INFORMATION:  
; APPLICANT: FRAZER, Ian  
; TITLE OF INVENTION: RECOMBINANT PAPILLOMA VIRUS L1  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,336  
; FILING DATE: 16-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/AU95/00292  
; FILING DATE: 17-MAY-1995  
; APPLICATION NUMBER: AU PM 5667  
; FILING DATE: 17-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 65064/118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-737-336-6

Query Match 100.0%; Score 55; DB 3; Length 532;  
Best Local Similarity 100.0%; Pred. No. 0.077; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 ICMGNOLFY 9  
DB 351 ICMGNOLFY 359

RESULT 9  
US-08-987-519-1  
Sequence 1, Application US/08987519  
Patent No. 5952216  
GENERAL INFORMATION:  
APPLICANT: Ludmerer, Steven  
TITLE OF INVENTION: Synthetic HPV16 Virus-like Particles  
FILE REFERENCE: 19853  
CURRENT APPLICATION NUMBER: US/08/987,519  
CURRENT FILING DATE: 1997-12-09  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 500  
TYPE: PR1  
ORGANISM: Human Papillomavirus  
US-08-987-519-1

Query Match 90.9%; Score 50; DB 2; Length 500;  
Best Local Similarity 88.9%; Pred. No. 0.51;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICMGNOLFY 9  
DB 320 ICMGNOLFY 328

RESULT 10  
US-08-987-519-3  
Sequence 3, Application US/08987519  
Patent No. 5952216  
GENERAL INFORMATION:  
APPLICANT: Ludmerer, Steven  
TITLE OF INVENTION: Synthetic HPV16 Virus-like Particles  
FILE REFERENCE: 19853  
CURRENT APPLICATION NUMBER: US/08/987,519  
CURRENT FILING DATE: 1997-12-09  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 501  
TYPE: PR1  
ORGANISM: Artificial Sequence  
FEATURES:  
NAME/KEY: SIMILAR  
LOCATION: (0)...(0)  
OTHER INFORMATION: Consensus Sequence  
OTHER INFORMATION: At 28 X = K or T  
OTHER INFORMATION: At 49 X = Y or F  
OTHER INFORMATION: At 53 X = K or R  
OTHER INFORMATION: At 54 X = V or A

OTHER INFORMATION: At 119 X = L or F  
OTHER INFORMATION: At 131 X = G or S  
OTHER INFORMATION: At 132 X = Y or No. 5952216Residue  
OTHER INFORMATION: At 170 X = T or K  
OTHER INFORMATION: At 173 X = S or T  
OTHER INFORMATION: At 176 X = S or P  
OTHER INFORMATION: At 179 X = L or A  
OTHER INFORMATION: At 219 X = L or I  
OTHER INFORMATION: At 225 X = V or T  
OTHER INFORMATION: At 246 X = Y or F  
OTHER INFORMATION: At 263 X = T or E  
OTHER INFORMATION: At 271 X = D or T  
OTHER INFORMATION: At 273 X = L or I  
OTHER INFORMATION: At 274 X = V or S  
OTHER INFORMATION: At 277 X = G or S  
OTHER INFORMATION: At 278 X = N or G  
OTHER INFORMATION: At 281 X = S or T  
OTHER INFORMATION: At 284 X = A or G  
OTHER INFORMATION: At 290 X = H or N  
OTHER INFORMATION: At 325 X = H or Q  
OTHER INFORMATION: At 346 X = S or T  
OTHER INFORMATION: At 347 X = K or T  
OTHER INFORMATION: At 348 X = A or S  
OTHER INFORMATION: At 366 X = F or Y  
OTHER INFORMATION: At 434 X = Q or P  
OTHER INFORMATION: At 439 X = D or L  
OTHER INFORMATION: At 440 X = M or L  
OTHER INFORMATION: At 458 X = F or Y  
OTHER INFORMATION: At 474 X = T or S  
OTHER INFORMATION: At 476 X = A or I  
OTHER INFORMATION: At 480 X = I or Y  
OTHER INFORMATION: At 488 X = P or A  
OTHER INFORMATION: At 490 X = T or A  
OTHER INFORMATION: At 497 X = T or R  
OTHER INFORMATION: At 501 X = K or R  
US-08-987-519-3

Query Match 89.1%; Score 49; DB 2; Length 501;  
Best Local Similarity 88.9%; Pred. No. 0.75;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICMGNOLFY 9  
DB 320 ICMGNOLFY 328

RESULT 11  
US-08-409-122-2  
Sequence 2, Application US/08409122  
Patent No. 5820870  
GENERAL INFORMATION:  
APPLICANT: JOYCE, JAMES G.  
APPLICANT: GEORGE, HUGH A.  
APPLICANT: HOFMANN, KATHRYN J.  
APPLICANT: JANSSEN, KATHRYN U.  
APPLICANT: NEPPER, MICHAEL P.  
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18 VACCINE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CHRISTINE E. CARRY - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,122  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/408,669  
FILING DATE: 22-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 19425  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-6734  
TELEFAX: 908-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 507 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-409-122-2

Query Match 85.5%; Score 47; DB 2; Length 507;  
Best Local Similarity 88.9%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
||| |||||  
Db 323 ICWGNOLFV 331

RESULT 12  
US-08-408-669-2  
Sequence 2, Application US/08408669  
Patent No. 5840306  
GENERAL INFORMATION:  
APPLICANT: HOFMANN, KATHRYN J.  
APPLICANT: JANSEN, KATHRYN U.  
APPLICANT: NEESEN, MICHAEL P.  
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,669  
FILING DATE: 22-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 19424  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-6734  
TELEFAX: 908-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-408-669-2

Query Match 85.5%; Score 47; DB 2; Length 507;  
Best Local Similarity 88.9%; Pred. No. 1.7;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
||| |||||  
Db 323 ICWGNOLFV 331

RESULT 13  
US-08-724-281-2  
Sequence 2, Application US/08724281  
Patent No. 5874089  
GENERAL INFORMATION:  
APPLICANT: SCHLEGEL, C. Richard  
APPLICANT: JENSON, A. Bennett  
APPLICANT: GHIM, Shin-Je  
TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,281  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,691  
FILING DATE: 02-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teekin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 010091-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-724-281-2

Query Match 78.2%; Score 43; DB 2; Length 503;  
Best Local Similarity 77.8%; Pred. No. 7.8;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ICWGNOLFV 9  
||| |||||  
Db 325 IAWGNOLFL 333

Mon Jul 21 18:20:12 2003

us-09-980-177a-12.rat

Page 6

RESULT 14  
US-08-622-354-3  
Sequence 3, Application US/08622354

Patent No. 5827518

GENERAL INFORMATION:

APPLICANT: WEBB, Bruce A.

APPLICANT: CUI, Liwang

TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE

TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: VA

COUNTRY: US

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/622,354

FILING DATE: 27-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 434-061

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 684-1111

TELEFAX: (703) 684-1124

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 322 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-622-354-3

Query Match 63.6%; Score 35; DB 2; Length 322;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGGNOLF 8  
DB 292 CWNKLF 298

RESULT 15

US-08-724-281-1

Sequence 1, Application US/08724281

Patent No. 5874089

GENERAL INFORMATION:

APPLICANT: SCHLEGEL, C. Richard

APPLICANT: JENSON, A. Bennett

APPLICANT: GHIM, Shin-Je

TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,281

FILING DATE: 01-OCT-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,691

FILING DATE: 02-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 010091-015

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 508 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-724-281-1

Query Match 61.8%; Score 34; DB 2; Length 508;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ICGNOLFV 9  
DB 330 ICGNOLFV 338

Search completed: July 17, 2003, 19:44:42  
Job time: 15 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2003, 19:44:26 ; Search time 307 Seconds  
(without alignments)  
18,901 Million cell updates/sec

Title: US-09-980-177a-12

Perfect score: 55  
Sequence: 1 ICWGNQLFV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/prodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*  
3: /cgn2\_6/prodata/1/paa/US07 COMB.pep.\*  
4: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*  
5: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*  
6: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*  
7: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*  
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27: /cgn2\_6/prodata/1/paa/US08 COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	494	21	US-09-791-537-16482	Sequence 16482, A
2	100.0	494	21	US-09-791-537-16490	Sequence 16490, A
3	100.0	494	21	US-09-791-537-16492	Sequence 16492, A
4	100.0	494	21	US-09-791-537-16493	Sequence 16493, A
5	100.0	494	21	US-09-791-537-16502	Sequence 16502, A
6	100.0	494	21	US-09-791-537-16503	Sequence 16503, A

7	55	100.0	494	21	US-09-791-537-16504	Sequence 16504, A
8	55	100.0	494	21	US-09-791-537-16513	Sequence 16513, A
9	55	100.0	494	21	US-09-791-537-16525	Sequence 16525, A
10	55	100.0	494	21	US-09-791-537-16527	Sequence 16527, A
11	55	100.0	494	21	US-09-791-537-16534	Sequence 16534, A
12	55	100.0	494	21	US-09-791-537-16549	Sequence 16549, A
13	55	100.0	495	21	US-09-791-537-16549	Sequence 16549, A
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15	55	100.0	500	1	PCT-US00-33549-17	Sequence 8, Appl1
16	55	100.0	500	1	US-09-791-537-84636	Sequence 17, Appl1
17	55	100.0	500	21	US-09-791-537-84645	Sequence 84645, A
18	55	100.0	500	21	US-09-791-537-84646	Sequence 84646, A
19	55	100.0	500	21	US-09-791-537-84647	Sequence 84647, A
20	55	100.0	500	21	US-09-791-537-84648	Sequence 84648, A
21	55	100.0	500	21	US-09-791-537-84654	Sequence 84654, A
22	55	100.0	500	21	US-09-791-537-84656	Sequence 84656, A
23	55	100.0	500	21	US-09-791-537-84658	Sequence 84658, A
24	55	100.0	500	21	US-09-791-537-112091	Sequence 112091, A
25	55	100.0	500	21	US-09-791-537-114229	Sequence 114229, A
26	55	100.0	500	21	US-09-791-537-117847	Sequence 117847, A
27	55	100.0	501	21	US-09-791-537-98351	Sequence 98351, A
28	55	100.0	503	21	US-09-791-537-67422	Sequence 67422, A
29	55	100.0	504	1	PCT-US00-33549-47	Sequence 47, Appl1
30	55	100.0	504	21	US-09-791-537-33220	Sequence 3220, Ap
31	55	100.0	504	21	US-09-791-537-117804	Sequence 117804, A
32	55	100.0	505	10	US-08-641-570-2	Sequence 2, Appl1
33	55	100.0	505	10	US-08-641-570-4	Sequence 4, Appl1
34	55	100.0	505	14	US-09-026-896-2	Sequence 2, Appl1
35	55	100.0	505	15	US-09-162-904-2	Sequence 2, Appl1
36	55	100.0	505	15	US-09-162-904-4	Sequence 4, Appl1
37	55	100.0	505	15	US-09-162-904A-3	Sequence 3, Appl1
38	55	100.0	505	15	US-09-162-904A-4	Sequence 4, Appl1
39	55	100.0	505	21	US-09-791-537-3195	Sequence 3195, Ap
40	55	100.0	505	21	US-09-791-537-5629	Sequence 5629, Ap
41	55	100.0	505	21	US-09-791-537-48978	Sequence 42978, A
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43	55	100.0	505	21	US-09-791-537-42981	Sequence 42981, A
44	55	100.0	505	21	US-09-791-537-51031	Sequence 51031, A
45	55	100.0	505	21	US-09-791-537-89377	Sequence 89377, A

#### ALIGNMENTS

RESULT 1  
US-09-791-537-16482  
; Sequence 16482, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomedix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 16482  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16482

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 ICWGNQLFV 9  
Db 314 ICWGNQLFV 322

RESULT 2  
US-09-791-537-16490  
; Sequence 16490, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16490  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16490

Query Match  
Best Local Similarity 100.0%; Score 55; DB 21; Length 494;  
Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9  
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Db 314 ICWGNOLFFV 322

RESULT 3  
US-09-791-537-16492  
; Sequence 16492, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16492  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16492

Query Match  
Best Local Similarity 100.0%; Score 55; DB 21; Length 494;  
Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9  
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Db 314 ICWGNOLFFV 322

RESULT 4  
US-09-791-537-16493  
; Sequence 16493, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16493

LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16493

Query Match  
Best Local Similarity 100.0%; Score 55; DB 21; Length 494;  
Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9  
| | | | | | | | | |  
Db 314 ICWGNOLFFV 322

RESULT 5  
US-09-791-537-16502  
; Sequence 16502, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16502  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16502

Query Match  
Best Local Similarity 100.0%; Score 55; DB 21; Length 494;  
Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9  
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Db 314 ICWGNOLFFV 322

RESULT 6  
US-09-791-537-16503  
; Sequence 16503, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16503  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16503

Query Match  
Best Local Similarity 100.0%; Score 55; DB 21; Length 494;  
Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOLFFV 9  
| | | | | | | | | |  
Db 314 ICWGNOLFFV 322

RESULT 7

US-09-791-537-16504  
; Sequence 16504, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16504  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16504

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOFLV 9  
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Db 314 ICWGNOFLV 322

RESULT 8  
US-09-791-537-16513  
; Sequence 16513, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16513  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16513

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOFLV 9  
|||  
Db 314 ICWGNOFLV 322

RESULT 9  
US-09-791-537-16525  
; Sequence 16525, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16525  
; LENGTH: 494

; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16525

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOFLV 9  
|||  
Db 314 ICWGNOFLV 322

RESULT 10  
US-09-791-537-16527  
; Sequence 16527, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16527  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16527

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOFLV 9  
|||  
Db 314 ICWGNOFLV 322

RESULT 11  
US-09-791-537-16534  
; Sequence 16534, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Biomimix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16534  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-791-537-16534

Query Match 100.0%; Score 55; DB 21; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNOFLV 9  
|||  
Db 314 ICWGNOFLV 322

RESULT 12  
US-09-791-537-16549

Mon Jul 21 18:20:13 2003

us-09-980-177a-12.rapm

Page 4

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Sequence 16549, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentn version 3.0
SEQ ID NO: 16549
LENGTH: 494
TYPE: PRT
ORGANISM: Human papillomavirus
US-09-791-537-16549
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Query Match          100.0%; Score 55; DB 21; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ICWGNQLFV 9
DB 314 ICWGNQLFV 322
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RESULT 13
US-09-791-537-42364
Sequence 42364, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentn version 3.0
SEQ ID NO: 42364
LENGTH: 495
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-791-537-42364
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Query Match          100.0%; Score 55; DB 21; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ICWGNQLFV 9
DB 317 ICWGNQLFV 325
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RESULT 14
PCT-US00-33549-8
Sequence 8, Application PC/TUS0033549
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
FILE REFERENCE: 018623-016110PC
CURRENT APPLICATION NUMBER: PCT/US00/33549
CURRENT FILING DATE: 2000-12-11
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PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/641,528
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 8
LENGTH: 500
TYPE: PRT
ORGANISM: Human papillomavirus type 6a
PCT-US00-33549-8
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Query Match          100.0%; Score 55; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ICWGNQLFV 9
DB 319 ICWGNQLFV 327
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RESULT 15
PCT-US00-33549-17
Sequence 17, Application PC/TUS0033549
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human
TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid
FILE REFERENCE: 018623-016110PC
CURRENT APPLICATION NUMBER: PCT/US00/33549
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/641,528
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 17
LENGTH: 500
TYPE: PRT
ORGANISM: Human papillomavirus type 6a
PCT-US00-33549-17
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Query Match          100.0%; Score 55; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ICWGNQLFV 9
DB 319 ICWGNQLFV 327
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Search completed: July 17, 2003, 19:52:59
Job time : 308 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2003, 19:42:36 ; Search time 40 Seconds  
(without alignments)  
21.630 Million cell updates/sec

Title: US-09-980-177a-12

Perfect score: 55

Sequence: 1 ICMGNQLFV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	55	100.0	500	1	PIWL6	L1 protein - human	
2	55	100.0	503	2	S36549	L1 protein - human	
3	55	100.0	504	1	PIWL31	L1 protein - human	
4	55	100.0	524	1	PIWL58	L1 protein - human	
5	55	100.0	529	2	S36578	L1 protein - human	
6	55	100.0	531	1	PIWLHS	major capsid prote	
7	55	100.0	534	2	S36583	L1 protein - human	
8	52	94.5	136	2	PC2225	peptide L1A6 3 - p	
9	52	94.5	499	1	PIWL3	L1 protein - human	
10	52	94.5	502	1	PIWL42	L1 protein - human	
11	52	94.5	508	2	S36508	L1 protein - human	
12	50	90.9	499	1	PIWL13	L1 protein - human	
13	50	90.9	501	1	PIWL11	L1 protein - human	
14	49	89.1	354	1	PIWLRI	L1 protein - human	
15	49	89.1	499	2	S36531	L1 protein - rhesu	
16	49	89.1	502	1	PIWL01	L1 protein - human	
17	49	89.1	502	2	S36526	L1 protein - pygmy	
18	49	89.1	503	2	S36514	L1 protein - human	
19	49	89.1	505	1	PIWL35	L1 protein - human	
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21	49	89.1	532	2	S36554	L1 protein (alters	
22	48	87.3	138	2	PC2224	peptide L1A6 2 - p	
23	48	87.3	504	1	PIWL51	L1 protein - human	
24	47	85.5	539	2	S36566	L1 protein - human	
25	46	83.6	138	2	PC2223	peptide L1A6 1 - p	
26	46	83.6	508	1	PIWL	L1 protein - human	
27	46	83.6	509	2	S36572	L1 protein - human	
28	46	83.6	517	2	S36496	L1 protein - human	
29	46	83.6	518	2	S36472	L1 protein - human	

30	46	83.6	546	2	S36490	L1 protein - human
31	46	83.6	568	1	PIWL18	L1 protein - human
32	45	81.8	501	1	PIWLEP	L1 protein - Euro
33	45	81.8	505	1	PIWLRB	L1 protein - cotto
34	45	81.8	505	2	S36589	L1 protein - human
35	45	81.8	505	2	S36560	L1 protein - human
36	44	80.0	505	1	PIWLPR	L1 protein - human
37	44	80.0	505	1	PIWL39	L1 protein - human
38	44	80.0	528	2	S36520	L1 protein - human
39	43	78.2	138	2	PC2226	peptide L1A6 4 - p
40	43	78.2	506	1	PIWLB4	L1 protein - bovin
41	43	78.2	507	2	S36595	L1 protein - human
42	43	78.2	507	2	S36484	L1 protein - human
43	43	78.2	510	1	S15627	L1 protein - human
44	43	78.2	594	2	S36502	L1 protein (alters
45	42	76.4	502	2	JB0295	L1 protein - human

## ALIGNMENTS

## RESULT 1

PIWL6  
L1 protein - human papillomavirus type 6b

C/Species: human papillomavirus type 6b

C/Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #ext\_change 16-Jul-1999

C/Accession: A03638

R/Schwarz, E.; Durr, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolferger, E.; St

EMBO J. 2, 2341-2346, 1983

A/Title: DNA sequence and genome organization of genital human papillomavirus type 6b.

A/Reference number: A90975; WUID:84131949; PMID:6321162

A/Accession: A03638

A/Molecule type: DNA

A/Residues: 1-500 <SCH>

A/Cross-references: GB:X00203; NID:G60955; PIDN:CAA25026.1; PID:G60964

C/Superfamily: papillomavirus L1 protein

C/Keywords: late protein

## Query Match

Best Local Similarity 100.0%; Score 55; DB 1; Length 500;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 319 ICMGNQLFV 327

## RESULT 2

S36549  
L1 protein - human papillomavirus type 26

C/Species: human papillomavirus type 26

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 26-Aug-1999

C/Accession: S36549

R/Dellus, H.; Hofmann, B.

A/Submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36549

A/Molecule type: DNA

A/Residues: 1-503 <DEL>

A/Cross-references: EMBL:X74472; NID:G396956; PIDN:CAA52535.1; PID:G396963

C/Superfamily: papillomavirus L1 protein

C/Keywords: late protein

## Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 503;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 323 ICMGNQLFV 331

RESULT 3  
P1WL31  
L1 protein - human papillomavirus type 31  
C:Species: human papillomavirus type 31  
A:Note: host Homo sapiens (man)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 16-Jul-1999  
R:Accession: G32444  
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.  
Virology 171, 306-311, 1989  
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-asso  
A:Reference number: A94398; MUID:89299478; PMID:2545036  
A:Accession: G32444  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-504 <GOL>  
A:Cross-references: GB:J04353; NID:G333048; PIDN:AAA46956.1; PID:G459922  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 100.0%; Score 55; DB 1; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.037;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||||  
Db 324 ICWGNQLFV 332

RESULT 4  
P1WL58  
L1 protein - human papillomavirus type 58  
C:Species: human papillomavirus type 58  
A:Note: host Homo sapiens (man)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jul-2000  
R:Accession: G36779  
R:Kiril, Y.; Iwamoto, S.; Matsukura, T.  
Virology 185, 424-427, 1991  
A:Title: Human papillomavirus type 58 DNA sequence.  
A:Reference number: A36779; MUID:92024102; PMID:1656594  
A:Accession: G36779  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-524 <KIR>  
A:Cross-references: GB:J09400; NID:G222386; PIDN:BA41851.1; PID:G3337104  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 100.0%; Score 55; DB 1; Length 524;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||||  
Db 349 ICWGNQLFV 357

RESULT 5  
S36378  
L1 protein - human papillomavirus type 52  
C:Species: human papillomavirus type 52  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S36578; I44889  
R:Deilus, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36578  
A:Molecule type: DNA  
A:Residues: 1-529 <DEL>  
A:Cross-references: EMBL:X74481; NID:G397038; PIDN:CA452590.1; PID:G397045  
R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Deilus, H.  
J. Clin. Microbiol. 30, 1716-1721, 1992  
A:Title: General primer polymerase chain reaction in combination with sequence analysis

A:Reference number: A44889; MUID:92332706; PMID:1321168  
A:Accession: I44889  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 368-399 <VAN>  
A:Cross-references: GB:S40277; NID:G251698; PIDN:AA82570.1; PID:G251699  
A:Experimental source: type Xa, cervical carcinoma in situ  
A:Note: sequence extracted from NCBI backbone (NCBIN:109399, NCBI:P.109447)  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 100.0%; Score 55; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||||  
Db 354 ICWGNQLFV 362

RESULT 6  
P1WLHS  
major capsid protein L1 - human papillomavirus type 16  
C:Species: human papillomavirus type 16  
C>Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 20-Aug-1999  
C:Accession: A03640; F44906; T10431  
C:Seedorf, K.; Kramer, G.; Duret, M.; Suhai, S.; Rowekamp, W.G.  
Virology 145, 181-185, 1985  
A:Title: Human papillomavirus type 16 DNA sequence.  
A:Reference number: A23355; MUID:85246220; PMID:2990099  
A:Accession: A03640  
A:Molecule type: DNA  
A:Residues: 1-531 <SE>  
A:Cross-references: GB:K02718; NID:G333031; PIDN:AAA46943.1; PID:G333037  
R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Deilus, H.  
J. Clin. Microbiol. 30, 1716-1721, 1992  
A:Title: General primer polymerase chain reaction in combination with sequence analysis  
A:Reference number: A44889; MUID:92332706; PMID:1321168  
A:Contents: mucosotropic type 16, cervical smear  
A:Accession: F44906  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 363-395 <VAN>  
A:Note: sequence extracted from NCBI backbone (NCBI:P.109407)  
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.  
J. Virol. 65, 2093-2097, 1991  
A:Title: A negative element in the human papillomavirus type 16 genome acts at the lev  
A:Reference number: 217014; MUID:91162763; PMID:1848319  
A:Accession: T10431  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-531 <KEN>  
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46943.1; PID:G333037  
C:Genetics:  
A:Gene: L1  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 100.0%; Score 55; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||||  
Db 349 ICWGNQLFV 357

RESULT 7  
S36583  
L1 protein - human papillomavirus type 56  
C:Species: human papillomavirus type 56  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S36583; H44889

R. Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36583  
A:Molecule type: DNA  
A:Residues: 1-534 <DEL>  
A:Cross-references: EMBL:X74463; NID:G397053; PIDN:CAA52600.1; PID:G397059  
R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Delius, H.  
J. Clin. Microbiol. 30, 1716-1721, 1992  
A:Title: General primer polymerase chain reaction in combination with sequence analysis  
A:Reference number: A44889; MUID:92332706; PMID:1321168  
A:Accession: H44889  
A:Molecule type: DNA  
A:Residues: 371-402 <VAN>  
A:Cross-references: GB:S40273; NID:G251696; PIDN:AAB22569.1; PID:G251697  
A:Experimental source: mucosotropic type 56, cervical smear  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:109398, NCBIIP:109406)  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 100.0%; Score 55; DB 2; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 357 ICMGNQLFV 365

RESULT 8  
PC2225  
peptide L1AE 3 - papillomavirus (fragment)

C:Species: papillomavirus  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-May-1997  
C:Accession: PC2225  
R:Tachezy, R.; Van Ranst, M.A.; Cruz, Y.; Burk, R.D.  
Biochem. Biophys. Res. Commun. 204, 820-827, 1994  
A:Title: Analysis of short novel human papillomavirus sequences.  
A:Reference number: PC2223; MUID:95071400; PMID:7980548  
A:Accession: PC2225  
A:Molecule type: DNA  
A:Residues: 1-136 <TAC>  
A:Cross-references: EMBL:U01533  
C:Superfamily: papillomavirus L1 protein

Query Match 94.5%; Score 52; DB 2; Length 136;  
Best Local Similarity 88.9%; Pred. No. 0.038;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 1 ICMGNQVFV 9

RESULT 9  
PIWL33

L1 protein - human papillomavirus type 33  
C:Species: human papillomavirus type 33  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Jul-1999  
C:Accession: A03641  
R:Cole, S.T.; Strebeck, R.E.  
J. Virol. 58, 991-995, 1986  
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, with  
A:Reference number: A93020; MUID:86200464; PMID:3009902  
A:Accession: A03641  
A:Molecule type: DNA  
A:Residues: 1-499 <COL>  
A:Cross-references: GB:M12732; NID:G333049; PIDN:AAA46964.1; PID:G463183  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 94.5%; Score 52; DB 1; Length 499;  
Best Local Similarity 88.9%; Pred. No. 0.13;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 323 ICMGNQVFV 331

RESULT 10

PIWL42  
L1 protein - human papillomavirus type 42  
C:Species: human papillomavirus type 42  
A:Note: host Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 27-Jan-1995  
C:Accession: G39451  
R:Phillips, W.; Honore, N.; Sapp, M.; Cole, S.T.; Strebeck, R.E.  
Virology 186, 331-334, 1992  
A:Title: Human papillomavirus type 42: new sequence, conserved genome organization.  
A:Reference number: A39451; MUID:92087479; PMID:1309278  
A:Accession: G39451  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-502 <PHI>  
A:Cross-references: GB:M73236  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 94.5%; Score 52; DB 1; Length 502;  
Best Local Similarity 88.9%; Pred. No. 0.13;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 323 ICMGNQFL 331

RESULT 11

S36508  
L1 protein - human papillomavirus type 30  
C:Species: human papillomavirus type 30  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S36508  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36508  
A:Molecule type: DNA  
A:Residues: 1-508 <DEL>  
A:Cross-references: EMBL:X74474; NID:G396973; PIDN:CAA52548.1; PID:G396980  
C:Superfamily: papillomavirus L1 protein  
C:Keywords: late protein

Query Match 94.5%; Score 52; DB 2; Length 508;  
Best Local Similarity 88.9%; Pred. No. 0.13;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 330 ICMGNQVFV 338

RESULT 12

PIWL13  
L1 protein - human papillomavirus type 13  
C:Species: human papillomavirus type 13  
A:Note: host Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Jul-1999  
C:Accession: H42955; A44889  
R:van Ranst, M.; Fuse, A.; Fliten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, C.  
Virology 190, 587-596, 1992  
A:Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar-

A:Reference number: A42955; MUID:92391075; PMID:1325697  
 A:Accession: H42955  
 A:Molecule type: DNA  
 A:Residues: 1-499 <VAN>  
 A:Cross-references: EMBL:X62843; NID:G60295; PIDN:CAA44654.1; PID:G60303  
 R:van den Brule, A.J.; Snijders, P.J.; Raaphorst, P.M.; Schrijnemakers, H.F.; Delius, H.  
 J. Clin. Microbiol. 30, 1716-1721, 1992  
 A:Title: General primer polymerase chain reaction in combination with sequence analysis  
 A:Reference number: A44889; MUID:92332706; PMID:1321168  
 A:Accession: A44889  
 A:Molecule type: DNA  
 A:Residues: 331-364 <VA2>  
 A:Cross-references: GB:S40235; NID:G251682; PIDN:AA622562.1; PID:G251683  
 A:Experimental source: microtropic type 13, cervical smear  
 A:Note: sequence extracted from NCBI Backbone (NCBIN:109389, NCBI:P.109410)  
 C:Superfamily: Papillomavirus L1 protein  
 C:Keywords: late protein

Query Match 90.9%; Score 50; DB 1; Length 499;  
 Best Local Similarity 88.9%; Pred. No. 0.29;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ICWGNOLFFV 9  
 |||||  
 Db 317 ICWGNHLEFV 325

RESULT 13  
 P1WLI1  
 L1 protein - human papillomavirus type 11  
 C:Species: human papillomavirus type 11  
 C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 16-Jul-1999  
 C:Accession: A03639  
 R:Partmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.  
 Virol. 151, 124-130, 1986  
 A:Title: The nucleotide sequence and genome organization of human papilloma virus type 11  
 A:Reference number: A94338; MUID:86181601; PMID:3008427  
 A:Accession: A03639  
 A:Molecule type: DNA  
 A:Residues: 1-501 <DAR>  
 A:Cross-references: GB:M14119; NID:G333026; PIDN:AAA46935.1; PID:G496201  
 C:Superfamily: papillomavirus L1 protein  
 C:Keywords: late protein

Query Match 90.9%; Score 50; DB 1; Length 501;  
 Best Local Similarity 88.9%; Pred. No. 0.29;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ICWGNOLFFV 9  
 |||||  
 Db 320 ICWGNHLEFV 328

RESULT 14  
 P1WLI1  
 L1 protein - rhesus papillomavirus (type 1)  
 C:Species: rhesus papillomavirus  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 27-Jan-1995  
 C:Accession: H38503  
 R:Ostrow, R.S.; Labresh, K.V.; Paras, A.J.  
 Virol. 181, 424-429, 1991  
 A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc  
 A:Reference number: A38503; MUID:91135018; PMID:1847267  
 A:Accession: H38503  
 A:Molecule type: DNA  
 A:Status: translation not shown  
 A:Residues: 1-354 <OST>  
 A:Cross-references: EMBL:M37717  
 C:Superfamily: papillomavirus L1 protein  
 C:Keywords: late protein

Query Match 89.1%; Score 49; DB 1; Length 354;  
 Best Local Similarity 77.8%; Pred. No. 0.31;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ICWGNOLFFV 9  
 |||||  
 Db 173 ICWGNOLFFV 181

RESULT 15  
 S36531  
 L1 protein - human papillomavirus type 53  
 C:Species: human papillomavirus type 53  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S36531  
 R:Delius, H.; Hofmann, B.  
 Submitted to the EMBL Data Library, August 1993.  
 A:Description: primer-directed sequencing of human papillomavirus types.  
 A:Reference number: S36469  
 A:Accession: S36531  
 A:Molecule type: DNA  
 A:Residues: 1-499 <DEL>  
 A:Cross-references: EMBL:X74482; NID:G397046; PIDN:CAA52595.1; PID:G397052  
 C:Superfamily: Papillomavirus L1 protein  
 C:Keywords: late protein

Query Match 89.1%; Score 49; DB 2; Length 499;  
 Best Local Similarity 88.9%; Pred. No. 0.43;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ICWGNOLFFV 9  
 |||||  
 Db 321 ICWGNOLFFV 329

Search completed: July 17, 2003, 19:46:52  
 Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 17, 2003, 19:42:31 ; Search time 24 Seconds  
(without alignments)  
15.554 Million cell updates/sec

Title: US-09-980-177a-12  
Sequence: 1 ICMGNQLFV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	152	VL1_HPV69	P50826 human papill
2	55	100.0	500	VL1_HPV44	P50816 human papill
3	55	100.0	500	VL1_HPV6A	P03100 human papill
4	55	100.0	501	VL1_HPV55	P50820 human papill
5	55	100.0	503	VL1_HPV26	P36738 human papill
6	55	100.0	504	VL1_HPV31	P17388 human papill
7	55	100.0	524	VL1_HPV58	P26535 human papill
8	55	100.0	529	VL1_HPV52	P05138 human papill
9	55	100.0	531	VL1_HPV16	P03101 human papill
10	55	100.0	534	VL1_HPV56	P36743 human papill
11	54	98.2	508	VL1_HPV60	P50821 human papill
12	53	96.4	150	VL1_HPV67	P50825 human papill
13	52	94.5	499	VL1_HPV43	P06416 human papill
14	52	94.5	502	VL1_HPV42	P27223 human papill
15	52	94.5	503	VL1_HPV46	P080961 human papill
16	52	94.5	508	VL1_HPV30	P02515 human papill
17	51	92.7	513	VL1_HPV48	P50817 human papill
18	50	90.9	489	VL1_HPV13	P02273 human papill
19	50	90.9	501	VL1_HPV11	P04012 human papill
20	49	89.1	497	VL1_HPV54	P50819 human papill
21	49	89.1	499	VL1_HPV53	P05113 human papill
22	49	89.1	501	VL1_RHPV1	P22163 rhesus papill
23	49	89.1	502	VL1_HPV28	P50791 human papill
24	49	89.1	502	VL1_HPV35	P27232 human papill
25	49	89.1	502	VL1_HPV35	P27232 human papill
26	49	89.1	503	VL1_PCPI1	P02274 PYGMY child
27	49	89.1	515	VL1_HPV32	P36737 human papill
28	49	89.1	531	VL1_HPV10	P36732 human papill
29	49	89.1	532	VL1_HPV03	P36731 human papill
30	48	87.3	504	VL1_HPV24	P26536 human papill
31	48	87.3	512	VL1_HPV24	P50790 human papill
32	48	87.3	516	VL1_HPV04	P07860 human papill
33	48	87.3	516	VL1_HPV04	P07860 human papill

34	47	85.5	539	1	VL1_HPV45	P36741 human papill
35	46	83.6	504	1	VL1_HPV70	P50793 human papill
36	46	83.6	508	1	VL1_HPV1A	P03099 human papill
37	46	83.6	509	1	VL1_HPV49	P36742 human papill
38	46	83.6	516	1	VL1_HPV20	P50786 human papill
39	46	83.6	517	1	VL1_HPV25	P02051 human papill
40	46	83.6	518	1	VL1_HPV14	P36734 human papill
41	46	83.6	518	1	VL1_HPV21	P50787 human papill
42	46	83.6	546	1	VL1_HPV19	P02050 human papill
43	46	83.6	568	1	VL1_HPV18	P06794 human papill
44	45	81.8	152	1	VL1_HPV43	P50815 human papill
45	45	81.8	501	1	VL1_PAPVE	P11326 european el

## ALIGNMENTS

```

RESULT 1
VL1_HPV69          STANDARD;          PRT;          152 AA.
ID
AC P50826;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 69.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37121;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95052821; PubMed=7963696;
RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,
RA Delius H., Beyron C.L., Bauer H.M., Wheeler C.M.;
RT "Identification and assessment of known and novel human
RT papillomaviruses by polymerase chain reaction amplification,
RT restriction fragment length polymorphisms, nucleotide sequence, and
RT phylogenetic algorithms."
RT J. Infect. Dis. 170:1077-1085(1994).
RL
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CC
DR EMBL: U12497; AAA67241.1; -
DR InterPro: IPR002210; PV_capsid.L1.
DR Pfam: PF00500; late_protein.L1; 1.
DR ProDom: PD000544; PV_capsid.L1; 1.
DR CoaT protein; late protein.
FT NON TER                               1
FT                                         152
SQ SEQUENCE 152 AA; 17269 MW; 8F7A927A8560656F CRC64;

Query Match          100.0%; Score 55; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9
Db 8 ICMGNQLFV 16

RESULT 2
VL1_HPV44          STANDARD;          PRT;          500 AA.
ID
AC P50816; Q80919;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

```

DT 15-JUL-1998 (Rel. 36, last annotation update)  
 DE Major capsid protein L1.  
 GN L1  
 OS Human papillomavirus type 44.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 CC Papillomavirus.  
 OX NCBI\_TaxID=10592;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Delius H.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 312-462 FROM N.A.  
 RX MEDLINE=95052821; PubMed=7963696;  
 RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,  
 RA Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;  
 RT "Identification and assessment of known and novel human  
 papillomaviruses by polymerase chain reaction amplification,  
 restriction fragment length polymorphisms, nucleotide sequence, and  
 phylogenetic algorithms.";  
 RT J. Infect. Dis. 170:1077-1085(1994).  
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 CC -----  
 DR EMBL: U12493; AAA67237.1; -  
 DR InterPro: IPR002210; PV\_capsid\_L1.  
 DR Pfam: PF00500; Late\_protein\_L1.  
 DR PRINTS: PR00865; HPVcapsid.L1.  
 DR ProDom: PD000544; PV\_capsid\_L1; 1.  
 DR Coat protein; Late protein.  
 SQ SEQUENCE 500 AA; 55849 MW; 277A4AB7CAA421F9 CRC64;  
 QY  
 Db 319 ICWGNQLFV 327  
 1 ICWGNQLFV 9  
 |||||  
 Query Match 100.0%; Score 55; DB 1; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RC SPECIES=Human papillomavirus type 6b;  
 RX MEDLINE=84131949; PubMed=6321152;  
 RA Schwarz E., Durst M., Demankowski C., Lattemann O., Zech R.,  
 RA Wolfesberger E., Subal S., Zur Hausen H.;  
 RT "DNA sequence and genome organization of genital human papillomavirus  
 type 6b";  
 RL EMO J. 2:2341-2348 (1983).  
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 CC -----  
 DR EMBL: L41216; AAA74218.1; -  
 DR EMBL: X00203; CAA25026.1; -  
 DR PIR: A03638; P1WL6.  
 DR InterPro: IPR002210; PV\_capsid\_L1.  
 DR Pfam: PF00500; Late\_protein\_L1.  
 DR PRINTS: PR00865; HPVcapsid.L1.  
 DR ProDom: PD000544; PV\_capsid\_L1; 1.  
 DR Coat protein; Late protein.  
 SQ SEQUENCE 500 AA; 55597 MW; B6168D0F76A287F7 CRC64;  
 QY  
 Db 319 ICWGNQLFV 327  
 1 ICWGNQLFV 9  
 |||||  
 Query Match 100.0%; Score 55; DB 1; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 VLI HPV55 STANDARD; PRT; 501 AA.  
 ID VLI HPV55  
 AC P50820; Q80940;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 15-JUL-1998 (Rel. 36, last annotation update)  
 DE Major capsid protein L1.  
 GN L1  
 OS Human papillomavirus type 55.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 CC Papillomavirus.  
 OX NCBI\_TaxID=37114;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Delius H.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 312-462 FROM N.A.  
 RX MEDLINE=95052821; PubMed=7963696;  
 RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,  
 RA Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;  
 RT "Identification and assessment of known and novel human  
 papillomaviruses by polymerase chain reaction amplification,  
 restriction fragment length polymorphisms, nucleotide sequence, and  
 phylogenetic algorithms.";  
 RT J. Infect. Dis. 170:1077-1085(1994).  
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 CC -----  
 DR EMBL: U31791; AAA79484.1; -  
 DR EMBL: U12494; AAA67238.1; -

DR InterPro: IPR002210; PV\_capsid\_L1.  
DR Pfam: PF00500; late\_protein\_L1; 1.  
DR PRINTS: PR00865; HPVcapsidL1.  
DR ProDom: PD000544; PV\_capsid\_L1; 1.  
KW Coat protein; late protein.  
SQ SEQUENCE 501 AA; 55787 MW; 0DBC4D47E552E368 CRC64;  
  
Query Match 100.0%; Score 55; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ICWGNOLEFV 9  
DB 319 ICWGNOLEFV 327  
  
RESULT 5  
VL1\_HPV26 STANDARD; PRT; 503 AA.  
ID VL1\_HPV26  
AC P36735;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Major capsid protein L1.  
GN L1.  
OS Human papillomavirus type 26.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
NCBI\_TaxID=31549;  
RN [1]  
RX SEQUENCE FROM N.A.  
RP MEDLINE=94265501; PubMed=8205838;  
RA Delius H., Hofmann B.;  
RT "Primer-directed sequencing of human papillomavirus types.";  
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
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CC -----  
CC EMBL: X74472; CA552535.1; -  
DR PIR: S36549; S36549.  
DR InterPro: IPR002210; PV\_capsid\_L1.  
DR Pfam: PF00500; late\_protein\_L1; 1.  
DR PRINTS: PR00865; HPVcapsidL1.  
DR ProDom: PD000544; PV\_capsid\_L1; 1.  
KW Coat protein; late protein.  
SQ SEQUENCE 503 AA; 56328 MW; A0706D12F425BB80 CRC64;  
  
Query Match 100.0%; Score 55; DB 1; Length 503;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ICWGNOLEFV 9  
DB 323 ICWGNOLEFV 331  
  
RESULT 6  
VL1\_HPV31 STANDARD; PRT; 504 AA.  
ID VL1\_HPV31  
AC P17388;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Major capsid protein L1.  
GN L1.  
OS Human papillomavirus type 31.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.  
OX NCBI\_TaxID=10585;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89299478; PubMed=2545036;  
RA Goldborough M.D., Dislivestre D., Temple G.F., Lorincz A.T.;  
RT "Nucleotide sequence of human papillomavirus type 31: a cervical  
RT neoplasia-associated virus";  
RL Virology 171:306-311(1989).  
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CC -----  
CC EMBL: J04353; AAA6956.1; -  
DR PIR: G32444; P1WL31.  
DR InterPro: IPR002210; PV\_capsid\_L1.  
DR Pfam: PF00500; late\_protein\_L1; 1.  
DR PRINTS: PR00865; HPVcapsidL1.  
DR ProDom: PD000544; PV\_capsid\_L1; 1.  
KW Coat protein; late protein.  
SQ SEQUENCE 504 AA; 56352 MW; B45A306A6B3AB9D2 CRC64;  
  
Query Match 100.0%; Score 55; DB 1; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ICWGNOLEFV 9  
DB 324 ICWGNOLEFV 332  
  
RESULT 7  
VL1\_HPV58 STANDARD; PRT; 524 AA.  
ID VL1\_HPV58  
AC P26535;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Major capsid protein L1.  
GN L1.  
OS Human papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
NCBI\_TaxID=10598;  
RN [1]  
RX SEQUENCE FROM N.A.  
RP MEDLINE=92024102; PubMed=1656594;  
RA Kiril Y., Iwamoto S., Matsukura T.;  
RT "Human papillomavirus type 58 DNA sequence";  
RL Virology 185:424-427(1991).  
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CC -----  
CC EMBL: D90400; BAA1851.1; -  
DR PIR: G36779; P1WL58.  
DR InterPro: IPR002210; PV\_capsid\_L1.  
DR Pfam: PF00500; late\_protein\_L1; 1.  
DR PRINTS: PR00865; HPVcapsidL1.  
DR ProDom: PD000544; PV\_capsid\_L1; 1.  
KW Coat protein; late protein.  
SQ SEQUENCE 524 AA; 59038 MW; 5DBC95E2878A26DF CRC64;

Query Match 100.0%; Score 55; DB 1; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ICMGNOL.FV 9  
 DB 349 ICMGNOL.FV 357

## RESULT 8

VL1\_HPV52 STANDARD; PRT; 529 AA.  
 AC C05138;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Major capsid protein L1.  
 GN L1.  
 OS Human papillomavirus type 52.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10618;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Delius H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 [2]  
 RN RP SEQUENCE OF 333-376 FROM N.A.  
 RX MEDLINE=92407963; PubMed=1326639;  
 RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Biggit H., Delius H.;  
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and  
 variants: a showcase for the molecular evolution of DNA viruses";  
 RL J. Virol. 66:5714-5725(1992).  
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 CC  
 CC EMBL; X74481; CA52590.1; -;  
 DR EMBL; M96287; AAA47036.1; -;  
 DR PIR; S36578; S36578;  
 DR InterPro; IPR002210; PV\_capsid\_L1;  
 DR Pfam; PF00500; late\_protein\_L1; 1.  
 DR PRINTS; PR00865; HPVcapsid.L1;  
 DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 KW Coat protein; Late protein.  
 SQ SEQUENCE 529 AA; 59469 MW; 77F7DB5CA964C53 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ICMGNOL.FV 9  
 DB 354 ICMGNOL.FV 362

## RESULT 9

VL1\_HPV16 STANDARD; PRT; 531 AA.  
 AC P03101;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Major capsid protein L1.  
 GN L1.  
 OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85246220; PubMed=2990099;  
 RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;  
 RT "Human papillomavirus type 16 DNA sequence.";  
 RL Virology 145:181-185(1985).  
 RN 12  
 RP SEQUENCE OF 328-371 FROM N.A.  
 RX MEDLINE=92407963; PubMed=1326639;  
 RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Biggit H., Delius H.;  
 RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and  
 variants: a showcase for the molecular evolution of DNA viruses";  
 RL J. Virol. 66:5714-5725(1992).  
 CC -1- MISCELLANEOUS: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE  
 OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.  
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 CC  
 CC EMBL; K02718; AAA46943.1; -;  
 DR EMBL; M96285; AAA47024.1; -;  
 DR EMBL; A06331; CAA00546.1; -;  
 DR PIR; A03640; P1WLHS;  
 DR InterPro; IPR002210; PV\_capsid\_L1.  
 DR Pfam; PF00500; late\_protein\_L1;  
 DR PRINTS; PR00865; HPVcapsid.L1;  
 DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 KW Coat protein; Late protein.  
 SQ SEQUENCE 531 AA; 59554 MW; 5B340258709B380 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ICMGNOL.FV 9  
 DB 349 ICMGNOL.FV 357

## RESULT 10

VL1\_HPV56 STANDARD; PRT; 534 AA.  
 AC P36743;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Major capsid protein L1.  
 GN L1.  
 OS Human papillomavirus type 56.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10596;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94265501; PubMed=8205838;  
 RA Delius H., Hofmann B.;  
 RT "Primer-directed sequencing of human papillomavirus types.";  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
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 CC  
 CC EMBL; X74481; CA52590.1; -;  
 DR EMBL; M96287; AAA47036.1; -;  
 DR PIR; S36578; S36578;  
 DR InterPro; IPR002210; PV\_capsid\_L1;  
 DR Pfam; PF00500; late\_protein\_L1; 1.  
 DR PRINTS; PR00865; HPVcapsid.L1;  
 DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 KW Coat protein; Late protein.  
 SQ SEQUENCE 529 AA; 59469 MW; 77F7DB5CA964C53 CRC64;



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 CC EMBL; X74483; CAA52600.1; -  
 CC DR PIR; S36583; S36583.  
 CC DR InterPro; IPR002210; PV\_capsid\_L1.  
 CC DR Pfam; PF00500; late\_protein\_L1; 1.  
 CC DR PRINTS; PR00865; HPVcapsidL1.  
 CC DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 CC KM Coat protein; late protein.  
 CC SQ SEQUENCE 534 AA; 60160 MW; 2ED3A965D1B1EC96 CRC64;  
 Query Match 100.0%; Score 55; DB 1; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ICWGNOLPV 9  
 DB 357 ICWGNOLPV 365  
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 RESULT 11  
 VLI\_HPV60 STANDARD; PRT; 508 AA.  
 AC P50821; Q80947;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Major capsid protein L1.  
 GN L1.  
 OS Human papillomavirus type 60.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCB1\_TaxID=40540;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Delius H.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RN SEQUENCE OF 372-467 FROM N.A.  
 RA Chan S.Y., Delius H., Halpern A.L., Bernard H.U.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; U11792; AAA79491.1; -  
 CC DR EMBL; U21876; AAA92837.1; -  
 CC DR InterPro; IPR002210; PV\_capsid\_L1.  
 CC DR Pfam; PF00500; late\_protein\_L1; 1.  
 CC DR PRINTS; PR00865; HPVcapsidL1.  
 CC DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 CC KM Coat protein; late protein.  
 CC SQ SEQUENCE 508 AA; 57827 MW; 3149549895534D00 CRC64;  
 Query Match 98.2%; Score 54; DB 1; Length 508;  
 Best Local Similarity 88.9%; Pred. No. 0.028;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ICWGNOLPV 9  
 DB 328 ICWGNOLPV 336  
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 RESULT 12  
 VLI\_HPV67 STANDARD; PRT; 150 AA.  
 AC P50825;  
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Major capsid protein L1 (Fragment).  
 GN L1.  
 OS Human papillomavirus type 67.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCB1\_TaxID=37120;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95052821; PubMed=7963696;  
 RA Bernard H.U., Chan S.Y., Manos M.M., Ong C.K., Villa L.L.,  
 RA Delius H., Peyton C.L., Bauer H.M., Wheeler C.M.;  
 RT "Identification and assessment of known and novel human  
 RT papillomaviruses by polymerase chain reaction amplification,  
 RT restriction fragment length polymorphisms, nucleotide sequence, and  
 RT phylogenetic algorithms.";  
 RL J. Infect. Dis. 170:1077-1085(1994).  
 CC -----  
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 CC -----  
 CC EMBL; U12482; AAA67236.1; -  
 CC DR InterPro; IPR002210; PV\_capsid\_L1.  
 CC DR Pfam; PF00500; late\_protein\_L1; 1.  
 CC DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 CC KM Coat protein; late protein.  
 CC FT NON\_TER 1 150  
 CC SQ SEQUENCE 150 AA; 17374 MW; 6ACBB50A47C5EB5B CRC64;  
 Query Match 96.4%; Score 53; DB 1; Length 150;  
 Best Local Similarity 88.9%; Pred. No. 0.014;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ICWGNOLPV 9  
 DB 8 ICWGNOLPV 16  
 -----  
 RESULT 13  
 VLI\_HPV33 STANDARD; PRT; 499 AA.  
 AC P06416;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Major capsid protein L1.  
 GN L1.  
 OS Human papillomavirus type 33.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCB1\_TaxID=10586;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86200464; PubMed=3009902;  
 RA Cole S.T., Strebeck R.E.;  
 RT "Genome organization and nucleotide sequence of human papillomavirus  
 RT type 33, which is associated with cervical cancer.";  
 RL J. Virol. 58:991-995(1986).  
 CC -----  
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 CC -----

```

CC EMBL; M12732; AAA46964.1;
DR PIR; A03641; P1WL33; PV_capsid_L1.
DR InterPro; IPR002210; late_protein_L1;
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsid_L1;
DR ProDom; PD000544; PV_capsid_L1;
DR Coat protein; Late protein.
SQ SEQUENCE 499 AA; 55902 MW; 283474DA93DE01D CRC64;

Query Match
Best Local Similarity 94.5%; Score 52; DB 1; Length 499;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9
Db 323 ICMGNQLFV 331

RESULT 14
VIL HPV42 STANDARD; PRT; 502 AA.
AC P2733;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major capsid protein L1.
OS Human papillomavirus type 42.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10590;
RN [1]
RX MBDLINE=92087479; PubMed=1309278;
RA Philipp W., Honore N., Sapp M., Cole S.T., Strebeck R.E.;
RT "Human papillomavirus type 42: new sequences, conserved genome
organization.";
RL Virology 186:331-334(1992).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73236; AAA47048.1; ALT_INT.
DR PIR; G39451; P1WL42.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsid_L1;
DR ProDom; PD000544; PV_capsid_L1;
DR Coat protein; Late protein.
SQ SEQUENCE 502 AA; 56165 MW; EDB083E650A1EA2E CRC64;

Query Match
Best Local Similarity 94.5%; Score 52; DB 1; Length 502;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9
Db 323 ICMGNQLFV 331

RESULT 15
VIL HPV42 STANDARD; PRT; 503 AA.
AC Q80961;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

```

```

DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 66.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37119;
RN [1]
RX MBDLINE=92087479; PubMed=1309278;
RA Philipp W., Honore N., Sapp M., Cole S.T., Strebeck R.E.;
RT "Human papillomavirus type 66: new sequences, conserved genome
organization.";
RL Virology 186:331-334(1992).
CC -----
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CC -----
CC EMBL; U31794; AAA79505.1;
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsid_L1;
DR ProDom; PD000544; PV_capsid_L1;
DR Coat protein; Late protein.
SQ SEQUENCE 503 AA; 56174 MW; 20649CE2E7875BA2 CRC64;

Query Match
Best Local Similarity 94.5%; Score 52; DB 1; Length 503;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9
Db 322 ICMGNQLFV 330

Search completed: July 17, 2003, 19:43:04
Job time : 25 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 17, 2003, 19:43:11 ; Search time 45 Seconds  
(without alignments)  
52.866 Million cell updates/sec

Title: US-09-980-177a-12

Perfect score: 55

Sequence: 1 ICWGNQLFV 9

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1232328 seqs, 264332421 residues

Total number of hits satisfying chosen parameters: 1232328

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents\_AA.New.\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	10	US-09-980-177a-12
2	55	100.0	10	10	US-09-641-528-2712
3	55	100.0	10	10	US-09-641-528-5468
4	55	100.0	10	10	US-09-641-528-8850
5	55	100.0	10	10	US-09-641-528-24989
6	55	100.0	10	10	US-09-641-528-27246
7	55	100.0	10	10	US-09-641-528-29966
8	55	100.0	10	10	US-09-641-528-2712
9	55	100.0	10	10	US-09-641-528-5468
10	55	100.0	10	10	US-09-641-528-8850
11	55	100.0	10	10	US-09-641-528-24989
12	55	100.0	10	10	US-09-641-528-27246
13	55	100.0	10	10	US-09-641-528-29966
14	55	100.0	10	10	US-09-641-528-2712
15	55	100.0	10	10	US-09-641-528-5468
16	55	100.0	10	10	US-09-641-528-8850
17	55	100.0	10	10	US-09-641-528-2712
18	55	100.0	10	10	US-09-641-528-5468
19	55	100.0	10	10	US-09-641-528-8850

20	55	100.0	20	10	US-09-980-177a-55	Sequence 55, Appl
21	55	100.0	500	12	US-10-149-136-8	Sequence 8, Appl
22	55	100.0	500	12	US-10-149-136-17	Sequence 17, Appl
23	55	100.0	504	12	US-10-149-136-47	Sequence 47, Appl
24	55	100.0	505	2	PCT-US03-04473-6	Sequence 6, Appl
25	55	100.0	505	2	PCT-US03-04516-6	Sequence 6, Appl
26	55	100.0	505	2	PCT-US03-04480-6	Sequence 6, Appl
27	55	100.0	505	2	PCT-US03-04474-6	Sequence 6, Appl
28	55	100.0	505	2	PCT-US03-04516A-6	Sequence 6, Appl
29	55	100.0	505	2	PCT-US03-04480A-6	Sequence 6, Appl
30	55	100.0	505	2	PCT-US03-04473A-6	Sequence 6, Appl
31	55	100.0	505	2	PCT-US03-04474A-6	Sequence 6, Appl
32	55	100.0	505	12	US-10-367-095-6	Sequence 6, Appl
33	55	100.0	505	12	US-10-367-043-6	Sequence 6, Appl
34	55	100.0	505	12	US-10-367-367-6	Sequence 6, Appl
35	55	100.0	505	12	US-10-368-046-6	Sequence 6, Appl
36	55	100.0	531	12	US-10-149-136-33	Sequence 33, Appl
37	55	100.0	531	12	US-10-301-260A-1	Sequence 1, Appl
38	55	100.0	534	12	US-10-149-136-65	Sequence 65, Appl
39	52	94.5	10	10	US-09-641-528-6818	Sequence 6818, Ap
40	52	94.5	10	10	US-09-641-528-28313	Sequence 28313, A
41	52	94.5	10	10	US-09-641-528A-6818	Sequence 6818, Ap
42	52	94.5	10	10	US-09-641-528A-28313	Sequence 28313, A
43	52	94.5	11	10	US-09-641-528-6819	Sequence 6819, Ap
44	52	94.5	11	10	US-09-641-528A-6819	Sequence 6819, Ap
45	52	94.5	499	12	US-10-149-136-60	Sequence 60, Appl

#### ALIGNMENTS

```

RESULT 1
US-09-980-177a-12
; Sequence 12, Application US/09980177A
; GENERAL INFORMATION:
; APPLICANT: Jochims, Ingrid
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DB 19925199.1
; PRIOR FILING DATE: 1999-06-01
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177a-12

Query Match          100.0%; Score 55; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ICWGNQLFV 9
        |||||
Db       1 ICWGNQLFV 9

RESULT 2
US-09-641-528-2712
; Sequence 2712, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban

```

APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2712  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-2712

Query Match 100.0%; Score 55; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 2 ICWGNQLFV 10

RESULT 3  
US-09-641-528-5468  
Sequence 5468, Application US/09641528  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5468  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-5468

Query Match 100.0%; Score 55; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 2 ICWGNQLFV 10

RESULT 4  
US-09-641-528-8850  
Sequence 8850, Application US/09641528  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Grey, Howard

TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8850  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-8850

Query Match 100.0%; Score 55; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 2 ICWGNQLFV 10

RESULT 5  
US-09-641-528-24989  
Sequence 24989, Application US/09641528  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24989  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-24989

Query Match 100.0%; Score 55; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
Db 2 ICWGNQLFV 10

RESULT 6  
US-09-641-528-27246  
Sequence 27246, Application US/09641528  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS

```

; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27246
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-27246

Query Match          100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ICMGNQLFV 9
        |||||
        2 ICMGNQLFV 10
```

```

RESULT 7
US-09-641-528-29966
; Sequence 29966, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29966
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-29966
```

```

Query Match          100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ICMGNQLFV 9
        |||||
        2 ICMGNQLFV 10
```

```

RESULT 8
US-09-641-528A-2712
; Sequence 2712, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
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; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2712
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-2712

Query Match          100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ICMGNQLFV 9
        |||||
        2 ICMGNQLFV 10
```

```

RESULT 9
US-09-641-528A-5468
; Sequence 5468, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5468
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-5468
```

```

Query Match          100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ICMGNQLFV 9
        |||||
        2 ICMGNQLFV 10
```

```

RESULT 10
US-09-641-528A-8850
; Sequence 8850, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
```

Mon Jul 21 16:20:14 2003

us-09-980-177a-12.rapn

Page 4

CURRENT APPLICATION NUMBER: US/09/641.528A  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 8850  
LENGTH: 10  
TYPE: PART  
ORGANISM: Artificial Sequence  
FEATURE: Peptide Derived from Human Papillomavirus  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528A-8850

Query Match Similarity 100.0%; Score 55; DB 10; Length 10;  
Seq Local Similarity 100.0%; Pred No. 0.015; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0

OY 1 ICWGNOLFFV 9  
DB 2 ICWGNOLFFV 10

RESULT 11  
US-09-641-528A-24989  
Sequence 24989, Application US/09641528A  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Sothwood, Robert  
APPLICANT: Chennouf, Robert  
APPLICANT: Celis, Eusebio  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.010001  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 24989  
LENGTH: 10  
TYPE: PART  
ORGANISM: Artificial Sequence  
FEATURE: Peptide Derived from Human Papillomavirus  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528A-24989

Query Match Similarity 100.0%; Score 55; DB 10; Length 10;  
Seq Local Similarity 100.0%; Pred No. 0.015; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0

OY 1 ICWGNOLFFV 9  
DB 2 ICWGNOLFFV 10

RESULT 12  
US-09-641-528A-27246  
Sequence 27246, Application US/09641528A  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Sothwood, Robert  
APPLICANT: Chennouf, Robert  
APPLICANT: Celis, Eusebio  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.010001  
CURRENT FILING DATE: 2000-08-15  
CURRENT APPLICATION NUMBER: US/09/641.528A

CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 27246  
LENGTH: 10  
TYPE: PART  
ORGANISM: Artificial Sequence  
FEATURE: Peptide Derived from Human Papillomavirus  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528A-27246

Query Match Similarity 100.0%; Score 55; DB 10; Length 10;  
Seq Local Similarity 100.0%; Pred No. 0.015; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0

OY 1 ICWGNOLFFV 9  
DB 2 ICWGNOLFFV 10

RESULT 13  
US-09-641-528A-29966  
Sequence 29966, Application US/09641528A  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Sothwood, Robert  
APPLICANT: Chennouf, Robert  
APPLICANT: Celis, Eusebio  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.010001  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51504  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 29966  
LENGTH: 10  
TYPE: PART  
ORGANISM: Artificial Sequence  
FEATURE: Peptide Derived from Human Papillomavirus  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528A-29966

Query Match Similarity 100.0%; Score 55; DB 10; Length 10;  
Seq Local Similarity 100.0%; Pred No. 0.015; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0

OY 1 ICWGNOLFFV 9  
DB 2 ICWGNOLFFV 10

RESULT 14  
US-09-641-528-2713  
Sequence 2713, Application US/09641528  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Sothwood, Robert  
APPLICANT: Chennouf, Robert  
APPLICANT: Celis, Eusebio  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
FILE REFERENCE: 2060.010001  
CURRENT FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51504  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 2713  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-2713

Query Match 100.0%; Score 55; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||  
Db 2 ICWGNQLFV 10

## RESULT 15

US-09-641-528-5469  
; Sequence 5469, Application US/09641528  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esleben  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; FILE REFERENCE: 2060.0100001  
; CURRENT APPLICATION NUMBER: US/09/641,528  
; CURRENT FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51504  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 5469  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528-5469

Query Match 100.0%; Score 55; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
|||  
Db 2 ICWGNQLFV 10

Search completed: July 17, 2003, 19:47:44  
Job time : 46 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 17, 2003, 19:42:36 ; Search time 77 Seconds  
(without alignments)  
24.083 Million cell updates/sec

Title: US-09-980-177a-12  
Perfect score: 55  
Sequence: 1 ICWGNQLFV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phase: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	44	12	084315 human papill
2	55	100.0	44	12	073442 human papill
3	55	100.0	44	12	073434 human papill
4	55	100.0	149	12	081054 human papill
5	55	100.0	149	12	081055 human papill
6	55	100.0	149	12	081056 human papill
7	55	100.0	149	12	081057 human papill
8	55	100.0	149	12	081058 human papill
9	55	100.0	149	12	081059 human papill
10	55	100.0	149	12	081059 human papill
11	55	100.0	150	12	081060 human papill
12	55	100.0	150	12	081061 human papill
13	55	100.0	150	12	081062 human papill
14	55	100.0	150	12	081063 human papill
15	55	100.0	150	12	081064 human papill
16	55	100.0	150	12	081065 human papill

17	55	100.0	150	12	011398 rhesus papi
18	55	100.0	151	12	012339 human papill
19	55	100.0	151	12	012340 human papill
20	55	100.0	151	12	012341 human papill
21	55	100.0	151	12	012342 human papill
22	55	100.0	151	12	084233 human papill
23	55	100.0	151	12	080996 human papill
24	55	100.0	494	12	080997 human papill
25	55	100.0	494	12	080998 human papill
26	55	100.0	494	12	080999 human papill
27	55	100.0	494	12	081000 human papill
28	55	100.0	494	12	081001 human papill
29	55	100.0	494	12	081002 human papill
30	55	100.0	494	12	081003 human papill
31	55	100.0	494	12	081004 human papill
32	55	100.0	494	12	081005 human papill
33	55	100.0	494	12	081006 human papill
34	55	100.0	494	12	081007 human papill
35	55	100.0	494	12	081008 human papill
36	55	100.0	494	12	081009 human papill
37	55	100.0	494	12	081010 human papill
38	55	100.0	494	12	081011 human papill
39	55	100.0	494	12	081012 human papill
40	55	100.0	494	12	090204 human papill
41	55	100.0	495	12	012343 human papill
42	55	100.0	500	12	099A88 human papill
43	55	100.0	500	12	099B85 human papill
44	55	100.0	500	12	099B86 human papill
45	55	100.0	500	12	099B87 human papill

## ALIGNMENTS

RESULT 1	ID	084315	PRELIMINARY;	PRT;	44 AA.
AC	084315;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	LI (Fragment).				
GN	LI.				
OS	Human papillomavirus type 56.				
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;				
OC	Papillomavirus.				
OX	NCBI_TaxId=10596;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92407963; PubMed=1326639;				
RA	Chan S.-Y., Bernard H.-U., Ong C.-K., Chan S.-P., Birgit H.,				
RA	Delius H.,				
RT	"Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and				
RT	variants: A showcase for the molecular evolution of DNA viruses.";				
RL	J. Virol. 66:5714-5725(1992).				
DR	EMBL; M96299; AAA47038.1; -				
DR	InterPro: IPR002210; PV_capsid_L1.				
DR	Pfam: PF00500; late_protein_L1; 1.				
DR	ProDom; PD000544; PV_capsid_L1; 1.				
FT	NON TER				
SQ	SEQUENCE 44 AA; 5028 MW; 3670DF29F5B1B48 CRC64;				
Query Match	100.0%; Score 55; DB 12; Length 44;				
Best Local Similarity	100.0%; Pred. No. 0.0035;				
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 ICWGNQLFV 9				
Db	22 ICWGNQLFV 30				
RESULT 2	073442				

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ID 073442 PRELIMINARY; PRT; 44 AA.
AC 073442;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=HAN 831;
RA Menzo S., Trozzi C., Clementi M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y12212; CAAT2885.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 44 AA; 5018 MW; B374F0B541507017 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ICWGNOLFY 9
1 ICWGNOLFY 9

RESULT 3
ID 073434 PRELIMINARY; PRT; 44 AA.
AC 073434;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 6.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=31552;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=HAN 1711;
RA Menzo S., Trozzi C., Clementi M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y12209; CAAT2882.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 44 AA; 5026 MW; 900B395B2006438 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ICWGNOLFY 9
1 ICWGNOLFY 9

RESULT 4
ID 081054 PRELIMINARY; PRT; 149 AA.
AC 081054;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10618;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=IS705;
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
RA Peto J., Wheeler C.M.;
RT "Intratype variation in 12 human papillomavirus types: a worldwide
RT perspective."
RL J. Virol. 70:3127-3136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IS705;
RA Farmer A.D.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45918; AAB19153.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 149 AA; 149 MW; 292758243B4B6A6C CRC64;

Query Match 100.0%; Score 55; DB 12; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ICWGNOLFY 9
8 ICWGNOLFY 16

RESULT 5
ID 081055 PRELIMINARY; PRT; 149 AA.
AC 081055;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10618;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=IS121;
RA MEDLINE=96186743; PubMed=8627792;
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
RA Peto J., Wheeler C.M.;
RT "Intratype variation in 12 human papillomavirus types: a worldwide
RT perspective."
RL J. Virol. 70:3127-3136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IS121;
RA Farmer A.D.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U45919; AAB19154.1;
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPVcapsidL1.
DR ProDom: PD000544; PV_capsid_L1; 1.
DR NON_TER 1
FT NON_TER 1

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FT NON\_TER 149 149  
SQ SEQUENCE 149 AA; 17162 MW; 292758243B4B6A6C CRC64;  
Query Match 100.0%; Score 55; DB 12; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ICMGNQLFV 9  
Db 8 ICMGNQLFV 16  
RESULT 6  
ID Q81056 PRELIMINARY; PRT; 149 AA.  
AC Q81056;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_Taxid=10618;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
Reto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
perspective.";  
RT J. Virol. 70:3127-3136(1996).  
RL J. Virol. 70:3127-3136(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS370;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45920; AAB19155.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 149 149  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 17162 MW; 292758243B4B6A6C CRC64;  
Query Match 100.0%; Score 55; DB 12; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ICMGNQLFV 9  
Db 8 ICMGNQLFV 16  
RESULT 7  
ID Q81057 PRELIMINARY; PRT; 149 AA.  
AC Q81057;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_Taxid=10618;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1001;

RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
Reto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
perspective.";  
RT J. Virol. 70:3127-3136(1996).  
RL J. Virol. 70:3127-3136(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1001;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45921; AAB19156.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 149 149  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 17162 MW; 292758243B4B6A6C CRC64;  
Query Match 100.0%; Score 55; DB 12; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ICMGNQLFV 9  
Db 8 ICMGNQLFV 16  
RESULT 8  
ID Q81058 PRELIMINARY; PRT; 149 AA.  
AC Q81058;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 52.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_Taxid=10618;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
Reto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
perspective.";  
RT J. Virol. 70:3127-3136(1996).  
RL J. Virol. 70:3127-3136(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1015;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45922; AAB19157.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 149 149  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 17162 MW; 292758243B4B6A6C CRC64;  
Query Match 100.0%; Score 55; DB 12; Length 149;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ICMGNQLFV 9  
Db 8 ICMGNQLFV 16

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RESULT 9
ID Q81059 PRELIMINARY; PRT; 149 AA.
AC Q81059;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS464;
RX MEDLINE=96186743; PubMed=8627792;
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
RA Peto J., Wheeler C.M.;
RT "Intratype variation in 12 human papillomavirus types: a worldwide
RT perspective.";
RL J. Virol. 70:3127-3136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IS464;
RA Farmer A.D.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45923; AB19158.1;
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT SEQUENCE 149 AA; 17177 MW; F61CD341916C448 CRC64;
SQ
Query Match 100.0%; Score 55; DB 12; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ICWGNQLEFV 9
Db 8 ICWGNQLEFV 16

RESULT 10
ID Q11399 PRELIMINARY; PRT; 149 AA.
AC Q11399;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rhesus monkey papillomavirus strain RHPV-K L1 (Fragment).
GN L1.
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10570;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RHEUS MONKEY PAPILLOMAVIRUS TYPE K;
RC Chan S.-Y., Bernard H.U., Ratteree M., Birkbeck T.A., Farras A.J.,
RA Ostrow R.S.;
RT "Genomic diversity and evolution of papillomaviruses in rhesus
RT monkeys.";
RL J. Virol. 0:0-0(1997).
RN [2]
RP EMBL; U89666; AAB63854.1;
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT SEQUENCE 149 AA; 17177 MW; F61CD341916C448 CRC64;
SQ

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FT NON_TER 149 149
SQ SEQUENCE 149 AA; 17163 MW; 398D45568FC00265 CRC64;
Query Match 100.0%; Score 55; DB 12; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ICWGNQLEFV 9
Db 8 ICWGNQLEFV 16

RESULT 11
ID Q81060 PRELIMINARY; PRT; 150 AA.
AC Q81060;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS068;
RX MEDLINE=96186743; PubMed=8627792;
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
RA Peto J., Wheeler C.M.;
RT "Intratype variation in 12 human papillomavirus types: a worldwide
RT perspective.";
RL J. Virol. 70:3127-3136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IS068;
RA Farmer A.D.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45924; AB19159.1;
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1;
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 1
FT SEQUENCE 150 AA; 17360 MW; 50378344223B1DBC CRC64;
SQ
Query Match 100.0%; Score 55; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ICWGNQLEFV 9
Db 8 ICWGNQLEFV 16

RESULT 12
ID Q81061 PRELIMINARY; PRT; 150 AA.
AC Q81061;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS573;

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RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
RA Peto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
RT perspective.";  
RL J. Virol. 70:3127-3136 (1996).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1021;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45925; AAB19160.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR Prodom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1 150  
FT NON\_TER 1 150  
SQ SEQUENCE 150 AA; 17360 MW; 503783442231BDBC CRC64;

Query Match 100.0%; Score 55; DB 12; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 8 ICMGNQLFV 16

RESULT 13  
ID Q81062 PRELIMINARY; PRT; 150 AA.  
AC Q81062;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OC NCBI\_TaxID=10598;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1021;  
RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
RA Peto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
RT perspective.";  
RL J. Virol. 70:3127-3136 (1996).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS1021;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45926; AAB19161.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR Prodom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1 150  
FT NON\_TER 1 150  
SQ SEQUENCE 150 AA; 17346 MW; AAB84539EBB1D4 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 8 ICMGNQLFV 16

RESULT 14  
ID Q81063 PRELIMINARY; PRT; 150 AA.  
AC Q81063;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OC NCBI\_TaxID=10598;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS131;  
RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
RA Peto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
RT perspective.";  
RL J. Virol. 70:3127-3136 (1996).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS131;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U45927; AAB19162.1; -;  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR Prodom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1 150  
FT NON\_TER 1 150  
SQ SEQUENCE 150 AA; 17360 MW; D23F29BE8035F352 CRC64;

Query Match 100.0%; Score 55; DB 12; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICMGNQLFV 9  
DB 8 ICMGNQLFV 16

RESULT 15  
ID Q81064 PRELIMINARY; PRT; 150 AA.  
AC Q81064;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 58.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OC NCBI\_TaxID=10598;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS404;  
RX MEDLINE=96186743; PubMed=8627792;  
RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,  
RA Peto J., Wheeler C.M.;  
RT "Intratype variation in 12 human papillomavirus types: a worldwide  
RT perspective.";  
RL J. Virol. 70:3127-3136 (1996).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=IS404;  
RA Farmer A.D.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U45928; AAB19163.1; -  
 DR InterPro; IPR002210; PV\_capsid\_L1.  
 DR Pfam; PF00500; late\_protein\_L1; 1.  
 DR PRINTS; PRO0865; HPVcapsid\_L1.  
 DR Prodom; PD000544; PV\_capsid\_L1; 1.  
 FT NON\_TER 1  
 FT NON\_TER 150  
 SQ SEQUENCE 150 AA; 17346 MW; 2883EF943CE5F34A CRC64;

Query Match 100.0%; Score 55; DB 12; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICWGNQLFV 9  
 |||||  
 DB 8 ICWGNQLFV 16

Search completed: July 17, 2003, 19:46:06  
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